```
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
        -50                 -45                 -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
    -35                 -30                 -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20                 -15                 -10                  -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                1                   5                  10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
        15                  20                  25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
    30                  35                  40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45                  50                  55                  60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
                65                  70                  75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
            80                  85                  90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
        95                  100                 105
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
    110                 115                 120
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
125                 130                 135                 140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
                145                 150                 155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
            160                 165                 170
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
        175                 180
```

<210> 171
<211> 350
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -68..-1

<400> 171

```
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
            -65                 -60                 -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
        -50                 -45                 -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
    -35                 -30                 -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20                 -15                 -10                  -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                1                   5                  10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
        15                  20                  25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
    30                  35                  40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45                  50                  55                  60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
                65                  70                  75
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
```

```
            80                  85                  90
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile
        95                  100                 105
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val
    110                 115                 120
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser
125                 130                 135                 140
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly
                145                 150                 155
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp
            160                 165                 170
Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
        175                 180                 185
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
    190                 195                 200
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
205                 210                 215                 220
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
                225                 230                 235
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
            240                 245                 250
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
        255                 260                 265
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
    270                 275                 280
```

<210> 172
<211> 390
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -68..-1

<400> 172

```
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
            -65                 -60                 -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
        -50                 -45                 -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
    -35                 -30                 -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20                 -15                 -10                 -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                1                   5                   10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
            15                  20                  25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
        30                  35                  40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45                  50                  55                  60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
                65                  70                  75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
            80                  85                  90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
        95                  100                 105
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
    1I0                 115                 120
```

```
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
125                 130                 135                 140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
                145                 150                 155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
            160                 165                 170
Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
        175                 180                 185
Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
    190                 195                 200
Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
205                 210                 215                 220
Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
                225                 230                 235
Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
            240                 245                 250
Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
        255                 260                 265
Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
    270                 275                 280
Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
285                 290                 295                 300
His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
                305                 310                 315
Glu Gly Thr Ser Ala Ser
            320
```

<210> 173
<211> 190
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -82..-1

<400> 173

```
Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
        -80                 -75                 -70
His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
    -65                 -60                 -55
Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile
-50                 -45                 -40                 -35
Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
                -30                 -25                 -20
Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
            -15                 -10                 -5
Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
        1                   5                   10
Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile
15                  20                  25                  30
Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
                35                  40                  45
Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu
            50                  55                  60
Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
        65                  70                  75
Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His
    80                  85                  90
Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
```

95 100 105

<210> 174
<211> 285
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -232..-1

<400> 174
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
-230 -225 -220
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
-215 -210 -205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
-200 -195 -190 -185
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
-180 -175 -170
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
-165 -160 -155
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
-150 -145 -140
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
-135 -130 -125
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
-120 -115 -110 -105
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
-100 -95 -90
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
-85 -80 -75
Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
-70 -65 -60
Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
-55 -50 -45
Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
-40 -35 -30 -25
Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
-20 -15 -10
Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
-5 1 5
Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
10 15 20
Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
25 30 35 40
Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys Lys
45 50

<210> 175
<211> 153
<212> PRT
<213> Homo sapiens

<400> 175
Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu

```
            20                  25                  30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
        35                  40                  45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
    50                  55                  60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65                  70                  75                  80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
                85                  90                  95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
            100                 105                 110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
        115                 120                 125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
    130                 135                 140
His His Cys Val Arg Glu Gly Ser Gly
145                 150
```

<210> 176
<211> 49
<212> PRT
<213> Homo sapiens

<400> 176

```
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
1               5                   10                  15
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
            20                  25                  30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
        35                  40                  45
Cys
```

<210> 177
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 177

```
Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
                -20                 -15                 -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
            -5                  1                   5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
    10                  15                  20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25                  30                  35                  40
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
                45                  50                  55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
            60                  65                  70
Pro Pro Arg
        75
```

<210> 178
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 178
Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
-35 -30 -25
Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
-20 -15 -10
Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
-5 1 5 10
Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
15 20 25
Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
30 35 40
Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
45 50 55

<210> 179
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 179
Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
-20 -15 -10
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
-5 1 5
Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
10 15 20 25
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
30 35 40
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
45 50 55
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
60 65 70
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
75 80 85
Gln Lys Leu Ala Lys Lys Met Phe Phe
90 95

<210> 180
<211> 59
<212> PRT
<213> Homo sapiens

<400> 180
Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg

```
1               5                   10                  15
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
            20                  25                  30
Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
        35                  40                  45
Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
    50                  55
```

<210> 181
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 181

```
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
                -10                 -5                  1
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
        5                   10                  15
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
    20                  25                  30
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
35                  40                  45                  50
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
                55                  60                  65
Tyr Arg Ile Cys Asp Leu
            70
```

<210> 182
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -58..-1

<400> 182

```
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
            -55                 -50                 -45
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
        -40                 -35                 -30
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
    -25                 -20                 -15
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
-10                 -5                  1                   5
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu
            10                  15                  20
Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
        25                  30                  35
Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
    40                  45                  50
Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
55                  60                  65                  70
Ser Leu Gln Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu
```

```
                75                  80                  85
Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
            90                  95                  100
Leu His Pro Trp Ala
        105
```

<210> 183
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 183

```
Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
-35                 -30                 -25                 -20
Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
                -15                 -10                 -5
Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
            1                   5                   10
Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
    15                  20                  25
Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
30                  35                  40                  45
```

<210> 184
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 184

```
Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
    -20                 -15                 -10
Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
-5                  1                   5                   10
Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys
            15                  20                  25
Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe
        30                  35                  40
Cys Gly Asn Ile Cys Met Ser Ile Leu
    45                  50
```

<210> 185
<211> 98
<212> PRT
<213> Homo sapiens

<400> 185

```
Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser
1               5                   10                  15
```

```
Ile Ser Lys Arg Glu Gln Leu Glu Gln Gln Val Pro Glu Asn Tyr Phe
            20                  25                  30
Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr
        35                  40                  45
Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp
    50                  55                  60
Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu
65                  70                  75                  80
Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
                85                  90                  95
Gly Tyr
```

<210> 186
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

```
<400> 186
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
    -20                 -15                 -10
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
-5                  1                   5                   10
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
            15                  20                  25
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro
        30                  35                  40
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
    45                  50                  55
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
60                  65                  70                  75
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
                80                  85                  90
```

<210> 187
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

```
<400> 187
Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro
                -40                 -35                 -30
Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe
            -25                 -20                 -15
Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His
        -10                 -5                  1
Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu
5                   10                  15                  20
Glu Trp Gly Leu Leu Arg
                25
```

<210> 188
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 188
Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser
-10 -5 1
Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe
5 10 15
Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln Gln Gln Pro Ser Ala Asn
20 25 30 35
Lys Lys Ala Gly Lys Ile His Asn Thr Pro Phe Ala Asn Gln Leu Asn
40 45 50
Pro Thr Gln His Leu Ala Lys Pro Phe Gln Gln Ile Leu Pro Gly Arg
55 60 65
Gln Ser Gly Ser Leu Thr Ser Pro Phe Leu Ala Cys
70 75

<210> 189
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 189
Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
-40 -35 -30
Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
-25 -20 -15
Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
-10 -5 1 5
Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
10 15 20
Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
25 30 35
Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
40 45 50
Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
55 60 65 70
Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile
75 80 85
Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
90 95 100
Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
105 110 115
Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
120 125 130
Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu
135 140 145 150
Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155 160 165

<210> 190
<211> 201
<212> PRT
<213> Homo sapiens

<400> 190
Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala Leu Lys Glu Lys Phe
1 5 10 15
Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe Gln Glu Ile Pro Lys
20 25 30
Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln Leu Glu Lys Ile Glu
35 40 45
Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile Asn Ile Thr Glu Met
50 55 60
Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val Asn His Leu Lys Ala
65 70 75 80
Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu Pro Thr Thr Val Glu
85 90 95
Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn Thr Leu Asn Ser Val
100 105 110
His Leu Ala Val Glu Ala Leu Gln Lys Thr Val Asp Glu His Lys Lys
115 120 125
Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln His Phe Leu Lys Glu
130 135 140
Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro Ser Ala Thr Ser Glu
145 150 155 160
Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys Gln Met Gly Asp Arg
165 170 175
Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln Val Thr Asn Arg Thr
180 185 190
Asp Thr Val Lys Ile Gln Lys Lys Lys
195 200

<210> 191
<211> 379
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 191
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
-35 -30 -25
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
-20 -15 -10
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
-5 1 5 10
Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
15 20 25
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
30 35 40
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
45 50 55
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

```
60                  65                  70                  75
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
                80                  85                  90
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
            95                  100                 105
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
        110                 115                 120
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
    125                 130                 135
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
140                 145                 150                 155
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
                160                 165                 170
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
            175                 180                 185
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
        190                 195                 200
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
    205                 210                 215
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
220                 225                 230                 235
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
                240                 245                 250
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
            255                 260                 265
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
        270                 275                 280
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
    285                 290                 295
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
300                 305                 310                 315
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Leu Ser Gly Met
                320                 325                 330
Gly Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
            335                 340
```

<210> 192
<211> 112
<212> PRT
<213> Homo sapiens

<400> 192

```
Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
1               5                   10                  15
Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
            20                  25                  30
Glu Asp Val Leu Glu Glu Cys Met Ser Leu Pro Lys Leu Ser Ser Tyr
        35                  40                  45
Ser Gly Trp Val Val Glu His Val Leu Pro His Met Gln Glu Asn Gln
    50                  55                  60
Pro Leu Ser Glu Thr Ser Pro Ser Ser Thr Ser Ala Ser Ala Leu Asp
65                  70                  75                  80
Gln Pro Ser Phe Val Pro Lys Ser Pro Asp Ala Ser Ser Ala Phe Ser
                85                  90                  95
Pro Ala Ser Pro Ala Thr Pro Asn Gly Thr Lys Gly Lys Lys Lys Lys
            100                 105                 110
```

<210> 193

<211> 43
<212> PRT
<213> Homo sapiens

<400> 193
Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser
1 5 10 15
Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn
20 25 30
Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
35 40

<210> 194
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 194
Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
-15 -10 -5
Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
1 5 10 15
Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
20 25 30
Pro Asn Phe
35

<210> 195
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 195
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
-15 -10 -5
Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
1 5 10
Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
15 20 25 30
Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
35 40 45
Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
50 55 60
Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
65 70 75
Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
80 85 90
Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
95 100 105 110
Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr

```
                115                 120                 125
Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
            130                 135                 140
Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
        145                 150                 155
Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
    160                 165                 170
Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
175                 180                 185                 190
His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val
                195                 200                 205
Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
            210                 215                 220
Arg Thr Ala Trp
        225
```

<210> 196
<211> 353
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 196

```
Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
                -30                 -25                 -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
            -15                 -10                 -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
        1                   5                   10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15                  20                  25                  30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
                35                  40                  45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
            50                  55                  60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr
        65                  70                  75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr
    80                  85                  90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly
95                  100                 105                 110
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met
                115                 120                 125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
            130                 135                 140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
        145                 150                 155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
    160                 165                 170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
175                 180                 185                 190
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
                195                 200                 205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
            210                 215                 220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
        225                 230                 235
```

```
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
    240                 245                 250
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
255                 260                 265                 270
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
                275                 280                 285
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
            290                 295                 300
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
        305                 310                 315
Leu
```

<210> 197
<211> 30
<212> PRT
<213> Homo sapiens

<400> 197
```
Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
1               5                   10                  15
Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys
            20                  25                  30
```

<210> 198
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -48..-1

<400> 198
```
Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
            -45                 -40                 -35
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
        -30                 -25                 -20
Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
    -15                 -10                 -5
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
1               5                   10                  15
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
            20                  25                  30
Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
        35                  40                  45
Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
    50                  55                  60
```

<210> 199
<211> 54
<212> PRT
<213> Homo sapiens

<400> 199
```
Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
1               5                   10                  15
```

```
Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
            20                  25                  30
Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
        35                  40                  45
Ser Ser Gly His Leu Pro
    50
```

<210> 200
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 200

```
Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val
    -20                 -15                 -10
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
-5                  1                   5                   10
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
            15                  20                  25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
        30                  35                  40
Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
    45                  50                  55
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
60                  65                  70                  75
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser Lys
                80                  85                  90
Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
            95                  100                 105
Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
        110                 115                 120
Gly Lys Val Lys Ser Phe Lys
    125                 130
```

<210> 201
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 201

```
Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
-25                 -20                 -15                 -10
Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
                -5                  1                   5
Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
        10                  15                  20
Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
    25                  30                  35
Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
40                  45                  50                  55
```

```
Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly
                60                  65                  70
Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
            75                  80                  85
Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly
        90                  95                  100
Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
    105                 110                 115
Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
120                 125                 130                 135
Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
                140                 145                 150
Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
            155                 160                 165
Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
        170                 175                 180
Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
    185                 190                 195
Asn Ala Tyr Val
200
```

<210> 202
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

```
<400> 202
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
        -45                 -40                 -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
    -30                 -25                 -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
-15                 -10                 -5                  1
Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
            5                   10                  15
```

<210> 203
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

```
<400> 203
Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly
    -30                 -25                 -20
Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile
-15                 -10                 -5                  1
Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys
            5                   10                  15
Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu
        20                  25                  30
```

```
Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn
    35                  40                  45
Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser
50                  55                  60                  65
Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe
                70                  75                  80
Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln
            85                  90                  95
Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys
        100                 105                 110
Lys Glu
    115
```

<210> 204
<211> 87
<212> PRT
<213> Homo sapiens

```
<400> 204
Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu
1               5                   10                  15
Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu
            20                  25                  30
Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu
        35                  40                  45
Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser
    50                  55                  60
Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu
65                  70                  75                  80
Glu Val Asp Asp Trp Glu Phe
                85
```

<210> 205
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

```
<400> 205
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
        -25                 -20                 -15
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
    -10                 -5                  1               5
Leu Ser Leu Arg Ser Ala Met Ser
                10
```

<210> 206
<211> 154
<212> PRT
<213> Homo sapiens

```
<400> 206
Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
```

```
1               5                   10                  15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
            20                  25                  30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
        35                  40                  45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
    50                  55                  60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
65                  70                  75                  80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
                85                  90                  95
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
            100                 105                 110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
        115                 120                 125
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
    130                 135                 140
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
145                 150
```

<210> 207
<211> 101
<212> PRT
<213> Homo sapiens

<400> 207

```
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
1               5                   10                  15
Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
            20                  25                  30
Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
        35                  40                  45
Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
    50                  55                  60
Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
65                  70                  75                  80
Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
                85                  90                  95
Lys Gln Thr Ser Val
            100
```

<210> 208
<211> 456
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 208

```
Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
        -20                 -15                 -10
Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
    -5                  1                   5                   10
Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
                15                  20                  25
Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser
```

```
            30                  35                  40
Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys Lys Ala Ser
        45                  50                  55
Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys Lys Lys Cys
    60                  65                  70
Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu Val Glu Arg
75                  80                  85                  90
Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp Ser Ala Glu
                95                  100                 105
Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro Ile Asn Ser
            110                 115                 120
Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys Ala Trp Lys
        125                 130                 135
Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly Ser Thr Ser
    140                 145                 150
Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg Asn Arg Gln
155                 160                 165                 170
Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro Gln Val Pro
                175                 180                 185
Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu Val Ser Pro
            190                 195                 200
Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala Leu Arg Ala
        205                 210                 215
Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr Leu Asn Glu
    220                 225                 230
Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu Phe Gln Glu
235                 240                 245                 250
Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln Ser Gln Val
                255                 260                 265
Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg Asp Leu Arg
            270                 275                 280
Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys Gly Asp Cys
        285                 290                 295
Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe Asp Leu Ala
    300                 305                 310
Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln Val Pro Leu
315                 320                 325                 330
Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser Leu Met Gly
                335                 340                 345
Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val Leu Lys Pro
            350                 355                 360
Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe Glu Asp Val
        365                 370                 375
Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys Ile Val Ser
    380                 385                 390
Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe Gln Lys Thr
395                 400                 405                 410
Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly Leu Gln Leu
                415                 420                 425
Gln Pro Cys Leu Tyr Lys Arg Arg
            430
```

<210> 209
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 209
Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
-15 -10 -5
Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
1 5 10 15
Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
20 25 30
Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
35 40 45
Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
50 55 60
Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
65 70 75
Val Glu
80

<210> 210
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 210
Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
-25 -20 -15
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
-10 -5 1
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
5 10 15
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
20 25 30 35
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
40 45 50
Asn Ala Ser

<210> 211
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 211
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

```
            45                  50                  55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
        60                  65                  70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
    75                  80                  85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
90                  95                  100                 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
                110                 115                 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
            125                 130                 135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
        140                 145                 150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
    155                 160                 165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
170                 175                 180                 185
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
                190                 195                 200
Arg Lys Ser Arg Thr
            205
```

<210> 212
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 212

```
Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
    -20                 -15                 -10
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
-5                  1                   5                   10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
            15                  20                  25
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
        30                  35                  40
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
    45                  50                  55
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
60                  65                  70                  75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
                80                  85                  90
Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
            95                  100                 105
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu
        110                 115                 120
Asn Asp Phe Ser Gln Glu Ser Ser
    125                 130
```

<210> 213
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 213
Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
-50 -45 -40
Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
-35 -30 -25
Ala Thr Pro Ser Ala Arg Ala Ala Ala Ala Val Val Ala Ala Ala Ala
-20 -15 -10
Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
-5 1 5 10
Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
15 20 25
Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu
30 35 40
Ala Gly Met Pro Ser Pro Glu Trp Thr Lys Arg Lys Lys Gln Thr Leu
45 50 55
Lys Ile Gly His Gly Gly Thr Leu Asp Ser Ala Ala Arg Gly Val Leu
60 65 70
Val Val Gly Ile Gly Ser Gly Thr Lys Met Leu Thr Ser Met Leu Ser
75 80 85 90
Gly Ser Lys Arg Tyr Thr Ala Ile Gly Glu Leu Gly Lys Ala Thr Asp
95 100 105
Thr Leu Asp Ser Thr Gly Lys Val Thr Glu Glu Lys Pro Tyr Gly Met
110 115 120
Asn Leu Ile
125

<210> 214
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -92..-1

<400> 214
Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu
-90 -85 -80
Leu Glu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro
-75 -70 -65
Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp
-60 -55 -50 -45
Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr
-40 -35 -30
Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala
-25 -20 -15
Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val
-10 -5 1
Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val
5 10 15 20
Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr Phe
25 30 35
Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu Cys
40 45 50
His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu Thr
55 60 65

```
Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn
    70                  75                  80
Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala
85                  90                  95                  100
Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln
                105                 110                 115
Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu
            120                 125                 130
His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala Asp
        135                 140                 145
Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu Thr
    150                 155                 160
Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
165                 170                 175
```

<210> 215
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 215

```
Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val
        -20                 -15                 -10
Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala
    -5                  1                   5                   10
Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser
                15                  20                  25
Phe Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile
            30                  35                  40
Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe
        45                  50                  55
His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu
    60                  65                  70
Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile
75                  80                  85                  90
Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn
                95                  100                 105
Ser Ala Pro Lys Ser Asn Val
            110
```

<210> 216
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 216

```
Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
            -35                 -30                 -25
Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
        -20                 -15                 -10
```

```
Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
    -5                   1                   5                  10
Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
                15                  20                  25
Glu Val Leu
```

<210> 217
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 217

```
Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
                -50                 -45                 -40
Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
            -35                 -30                 -25
Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
        -20                 -15                 -10
Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
    -5                  1                   5                  10
Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
                15                  20                  25
Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
            30                  35                  40
Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
        45                  50                  55
Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
    60                  65                  70
```

<210> 218
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 218

```
Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
    -20                 -15                 -10
Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
-5                  1                   5                  10
Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
            15                  20                  25
Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
        30                  35                  40
Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
    45                  50                  55
Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
60                  65                  70                  75
Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe
                80                  85                  90
Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln Thr Lys
```

```
            95                  100                 105
Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys Leu Leu
        110                 115                 120
Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly Thr Leu
    125                 130                 135
Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala Val Asp
140                 145                 150                 155
Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala Leu Thr
                160                 165                 170
Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp Asn His
            175                 180                 185
Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp Leu Val
        190                 195                 200
Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser Trp Leu
    205                 210                 215
Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe Gln Val
220                 225                 230                 235
Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys Pro Trp
                240                 245                 250
Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro Val Ala
            255                 260                 265
Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg Ile Gln
        270                 275                 280
Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro Leu Pro
    285                 290                 295
Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val Ser Gly
300                 305                 310                 315
Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly Gly His
                320                 325                 330
Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu Ala Gln
            335                 340                 345
Arg Ser Tyr Leu Pro Gln Ile Ser
        350                 355
```

<210> 219
<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 219

```
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
-30                 -25                 -20                 -15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
                -10                 -5                  1
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
        5                   10                  15
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
    20                  25                  30
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
35                  40                  45                  50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                55                  60                  65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met
            70                  75                  80
Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe
        85                  90                  95
```

```
His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
    100                 105                 110
Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
115                 120                 125                 130
Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
                135                 140                 145
Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
            150                 155                 160
Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
        165                 170                 175
Arg Gln Leu
    180
```

<210> 220
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -60..-1

<400> 220

```
Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
-60                  -55                 -50                 -45
Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
                -40                 -35                 -30
Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
            -25                 -20                 -15
Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
        -10                 -5                  1
Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
5                   10                  15                  20
Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
                25                  30                  35
Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
            40                  45                  50
Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
        55                  60                  65
Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
    70                  75                  80
Pro Glu Phe His Ile Glu Ile Leu Ser Ile
85                  90
```

<210> 221
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 221

```
Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
        -40                 -35                 -30
Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
    -25                 -20                 -15
```

```
Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
-10                 -5                   1                   5
Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser
            10                  15                  20
Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser
        25                  30                  35
Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Thr Ala Arg Ala Leu
    40                  45                  50
Cys Leu Gly Cys Ser Cys Cys Thr Glu Arg Leu Leu Leu Pro Pro Pro
55                  60                  65                  70
Ser Leu Leu Ser Leu Glu Ala Pro Ala Ser Thr
                75                  80
```

<210> 222
<211> 346
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 222

```
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
                -15                 -10                 -5
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
            1               5                   10
Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
    15                  20                  25
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
30                  35                  40                  45
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
                50                  55                  60
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
            65                  70                  75
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
        80                  85                  90
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
    95                  100                 105
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
110                 115                 120                 125
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
                130                 135                 140
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
            145                 150                 155
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
        160                 165                 170
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
    175                 180                 185
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
190                 195                 200                 205
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
                210                 215                 220
His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
            225                 230                 235
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
        240                 245                 250
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
    255                 260                 265
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
```

```
270                 275                 280                 285
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
                290                 295                 300
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
            305                 310                 315
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
        320                 325
```

<210> 223
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 223

```
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20                 -15                 -10                 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
                1                   5                   10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
        15                  20                  25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
    30                  35                  40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45                  50                  55                  60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
                65                  70                  75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
            80                  85                  90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
        95                  100                 105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
    110                 115                 120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
125                 130                 135                 140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
                145                 150                 155
His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu
            160                 165                 170
Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys
        175                 180                 185
Pro Lys
    190
```

<210> 224
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 224

```
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
```

```
-20                 -15                 -10                 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
                1                   5                   10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
        15                  20                  25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
    30                  35                  40
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
45                  50                  55                  60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
                65                  70                  75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
            80                  85                  90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
        95                  100                 105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
    110                 115                 120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
125                 130                 135                 140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
                145                 150                 155
His Leu Leu Ala Asp Thr Met Leu
            160
```

<210> 225
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 225

```
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
        -20                 -15                 -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
    -5                  1                   5                   10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
                15                  20                  25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
            30                  35                  40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
        45                  50                  55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
    60                  65                  70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
75                  80                  85                  90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
                95                  100                 105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
            110                 115                 120
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
        125                 130                 135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
    140                 145                 150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
155                 160                 165                 170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
                175                 180                 185
```

```
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
            190                 195                 200
Ala Ala Cys
        205
```

<210> 226
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 226

```
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
    -40                 -35                 -30
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
-25                 -20                 -15                 -10
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
                -5                  1                   5
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
        10                  15                  20
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
    25                  30
```

<210> 227
<211> 73
<212> PRT
<213> Homo sapiens

<400> 227

```
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
1               5                   10                  15
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
            20                  25                  30
Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met Val Lys Lys Ile Ala
        35                  40                  45
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
    50                  55                  60
Asn Leu Leu Glu Val Cys Lys Lys Lys
65                  70
```

<210> 228
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 228

```
Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
    -15                 -10                 -5
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
```

```
1               5                   10                  15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
            20                  25                  30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
        35                  40                  45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
    50                  55                  60
Lys Asn
65
```

<210> 229
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56..-1

<400> 229

```
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
    -55                 -50                 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40                 -35                 -30                 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
                -20                 -15                 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
            -5                  1                   5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
    10                  15                  20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25                  30                  35                  40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
                45                  50                  55
Ile Leu Ala Lys Lys Lys Lys
            60
```

<210> 230
<211> 54
<212> PRT
<213> Homo sapiens

<400> 230

```
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1               5                   10                  15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
            20                  25                  30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
        35                  40                  45
Gly Arg Gly Arg Pro His
    50
```

<210> 231
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 231
Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
-10 -5 1
Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
5 10 15
Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
20 25 30
Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
35 40 45 50
Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
55 60 65
Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met
70 75 80
Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
85 90 95
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
100 105 110
Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
115 120 125 130
Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
135 140 145
Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
150 155 160
Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
165 170 175
Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
180 185 190
Gln Glu
195

<210> 232
<211> 108
<212> PRT
<213> Homo sapiens

<400> 232
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20 25 30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35 40 45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50 55 60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65 70 75 80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85 90 95
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
100 105

<210> 233
<211> 43

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 233
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
-15 -10 -5
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
1 5 10
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
15 20 25

<210> 234
<211> 36
<212> PRT
<213> Homo sapiens

<400> 234
Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
1 5 10 15
Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
20 25 30
Phe Phe Gln Ile
35

<210> 235
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 235
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
-10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
40 45 50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
55 60 65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
70 75 80
Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
85 90 95
Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu
100 105 110 115
Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
120 125 130
Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
135 140 145

```
Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
        150                 155                 160
Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
    165                 170                 175
Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
180                 185                 190                 195
Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
                200                 205                 210
Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
            215                 220                 225
Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
        230                 235                 240
Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
    245                 250                 255
Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
260                 265                 270                 275
Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
                280                 285                 290
Lys Lys Lys
```

<210> 236
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 236

```
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
        -30                 -25                 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
    -15                 -10                 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1                   5                   10                  15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
            20                  25                  30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
        35                  40                  45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
    50                  55                  60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65                  70
```

<210> 237
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 237

```
Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
                -15                 -10                 -5
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
```

```
            1               5                   10
Gln Leu Ser Asp Lys Val His Asn Asp Ile
    15                  20
```

<210> 238
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 238

```
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
-20                 -15                 -10                 -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
                 1                   5                  10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
        15                  20                  25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
    30                  35                  40
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
45                  50                  55                  60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
                65                  70                  75
Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile
            80                  85                  90
Ile Asp Lys Thr Thr
        95
```

<210> 239
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 239

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Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
        -35                 -30                 -25
Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile
    -20                 -15                 -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
-5                  1                   5                  10
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
            15                  20                  25
Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
        30                  35                  40
Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
    45                  50                  55
Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
60                  65                  70                  75
His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
                80                  85                  90
Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe
```

```
            95                  100                 105
His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
        110                 115                 120
Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
    125                 130                 135
Ile Gly
140
```

<210> 240
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 240

```
Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val
        -25                 -20                 -15
Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser
    -10                 -5                  1                   5
Met Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe Ile
                10                  15                  20
Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala
            25                  30                  35
Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
        40                  45                  50
Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met Lys Gly
    55                  60                  65
Leu Lys Cys Arg Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro
70                  75                  80                  85
Tyr Phe Lys Met His Lys Pro Val Thr Met Lys Lys Lys Lys
                90                  95
```

<210> 241
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -115..-1

<400> 241

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Met Arg Trp Ser Cys Glu His Leu Val Met Val Trp Ile Asn Ala Phe
-115                 -110                 -105                 -100
Val Met Leu Thr Thr Gln Leu Leu Pro Ser Lys Tyr Cys Asp Leu Leu
                -95                  -90                  -85
His Lys Ser Ala Ala His Leu Gly Lys Trp Gln Lys Leu Glu His Gly
            -80                  -75                  -70
Ser Tyr Ser Asn Ala Pro Gln His Ile Trp Ser Glu Asn Thr Ile Trp
        -65                  -60                  -55
Pro Gln Gly Val Leu Val Arg His Ser Arg Cys Leu Tyr Arg Ala Met
    -50                  -45                  -40
Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg Phe
-35                  -30                  -25                  -20
Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile Leu
```

```
                -15                 -10                 -5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser
            1               5                   10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn
    15                  20                  25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg
30                  35                  40                  45
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn
                50                  55
```

<210> 242
<211> 896
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..173

<221> sig_peptide
<222> 18..77
<223> Von Heijne matrix
score 6.5
seq GLCVLQLTTAVTS/AF

<221> polyA_signal
<222> 864..869

<221> polyA_site
<222> 882..893

<400> 242

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aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc        50
                   Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
                   -20                 -15                 -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg        98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
                -5                  1                   5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc       146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
        10                  15                  20
cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcctgattca            193
His His Phe Ile His Pro Cys Leu Asp
    25                  30
aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgcttcag    253
agagggcagc acttatacct ggtggtcttt ctgatggtca gttttattcc cctcctgaat    313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaacca cttttagaac    373
tatgagtact acttttgtta aatgtgaaaa accctcacag aaagtcatcg aggcaaaaag    433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atggtgacgt ccactgctgg    493
ctttattgaa cagctaataa agatttattt attgtaatac ctcacagacg ttgtaccata    553
tccatgcaca tttagttgcc tgcctgtggc tggtaaggta atgtcatgat tcatcctctc    613
ttcagtgaga ctgagcctga tgtgttaaca aataggtgaa gaaagtcttg tgctgtattc    673
ctaatcaaaa gacttaatat attgaagtaa cacttttta gtaagcaaga taccttttta    733
tttcaattca cagaatggaa ttttttgtt tcatgtctca gatttatttt gtatttcttt    793
tttaacactc tacatttccc ttgttttta actcatgcac atgtgctctt tgtacagttt    853
taaaaagtgt aataaaatct gacatgtcaa araaaaaaaa mcy                     896
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<210> 243

<211> 851
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..595

<221> sig_peptide
<222> 17..85
<223> Von Heijne matrix
score 3.70000004768372
seq FLPPLXRAFACRG/CQ

<221> polyA_signal
<222> 820..825

<221> polyA_site
<222> 840..851

<400> 243
aaggggcgt ggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc 52
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
-20 -15
ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg 100
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
-10 -5 1 5
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga 148
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
10 15 20
ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat 196
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
25 30 35
aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa 244
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
40 45 50
tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa 292
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
55 60 65
tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa 340
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
70 75 80 85
aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg 388
Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu
90 95 100
aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg 436
Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala
105 110 115
gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat 484
Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr
120 125 130
tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg 532
Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met
135 140 145
gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa 580
Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln
150 155 160 165
aag aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac 635
Lys Lys Arg Ser Asn
170
aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga 695
agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggtag gtcctggggc 755

```
actgtgggcc gcctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtacgtggt    815
gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa                              851
```

<210> 244
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..334

<221> sig_peptide
<222> 89..130
<223> Von Heijne matrix
score 3.59999990463257
seq AFTLXSLLQAALL/CV

<221> polyA_signal
<222> 462..467

<221> polyA_site
<222> 484..495

<400> 244

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agtaggaasg cgccgsccgt ggaggcgcca cgtcccttgc sgcggcggga gagamatcgc     60
ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg       112
                                 Met Ala Phe Thr Leu Xaa Ser Leu
                                                 -10
ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag      160
Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
    -5                  1               5                  10
gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt      208
Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
                15                  20                  25
gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att      256
Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
            30                  35                  40
cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca      304
Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
        45                  50                  55
att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaat        354
Ile Ala Ile Val Leu Leu Leu Leu Phe Gly
    60                  65
ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt    414
atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaat aaaaccaggg    474
tttctattta aaaaaaaaaa a                                             495
```

<210> 245
<211> 884
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..614

<221> sig_peptide

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<222> 21..83
<223> Von Heijne matrix
      score 10
      seq LWALAMVTRPASA/AP

<221> polyA_signal
<222> 849..854

<221> polyA_site
<222> 873..884

<400> 245
aataccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc     53
                    Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
                   -20                 -15
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      101
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
-10                 -5                  1               5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg      149
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
            10                  15                  20
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg      197
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg
        25                  30                  35
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa      245
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
    40                  45                  50
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt      293
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
55                  60                  65                  70
cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg      341
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu
                75                  80                  85
cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car      389
Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
            90                  95                  100
aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc      437
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa
        105                 110                 115
gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc      485
Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro
    120                 125                 130
cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak      533
Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa
135                 140                 145                 150
cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc      581
Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile
                155                 160                 165
cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac    634
Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala
            170                 175
tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggcccct gtgcagggag    694
gagctgcctg ttcactggga tcagccaggg cgccgggccc cacttctgag cacagagcar    754
agacagacgc aggcggggac aaaggcagag gatgtagccc cattggggag gggtggagga    814
aggacatgta ccctttcatr mctacacacc cctcattaaa gcavagtcgt ggcatctcaa    874
aaaaaaaaaa                                                          884


<210> 246
<211> 897
<212> DNA
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<213> Homo sapiens

<220>
<221> CDS
<222> 94..573

<221> sig_peptide
<222> 94..258
<223> Von Heijne matrix
score 4.69999980926514
seq IGILCSLLGTVLL/WV

<221> polyA_signal
<222> 862..867

<221> polyA_site
<222> 886..897

<400> 246

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aagggcggct gcctagcacc cggaagagcc gtcaacttag cgagcgcaac aggctgccgc      60
tgaggagctg gagctggtgg ggactgggcc gca atg gac aag ctg aag aag gtg      114
                                      Met Asp Lys Leu Lys Lys Val
                                      -55                 -50
ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
            -45                 -40                 -35
gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
        -30                 -25                 -20
tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
    -15                 -10                 -5
tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1               5                   10                  15
ggt aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
            20                  25                  30
aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
        35                  40                  45
atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
    50                  55                  60
cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                  70                  75                  80
ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
                85                  90                  95
aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat            593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
            100                 105
gaagctttgg aaggcactat ggacagaagc tggtggacag ttttgtwact atcttcgaaa     653
cctctgtctt acagacatgt gccttttatc ttgcagcaat gtgttgcttg tgattcgaac     713
atttgagggt tacttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag     773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcatgtacc tgtttcctct     833
ctggatgttg tcccactgaa ttcccatgaa tacaaaccta ttcagcaaca gcaaaaaaaa     893
aaaa                                                                 897
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<210> 247
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..397

<221> sig_peptide
<222> 74..127
<223> Von Heijne matrix
score 7.69999980926514
seq LLLLPVLGLLVSS/KT

<221> polyA_signal
<222> 472..477

<221> polyA_site
<222> 507..518

<400> 247
aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggttagctga gcccaccgag 60
aggcgcctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg 109
Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
-15 -10
ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
-5 1 5 10
aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
15 20 25
agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
30 35 40
gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
45 50 55
gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
60 65 70
tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc 397
Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
75 80 85 90
tgaggtcgcg cgcagcgcgt gcacagcgcg ggcggaggcg gctccaggtc cggaggggtt 457
gcgggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa 517
a 518

<210> 248
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..242

<221> sig_peptide
<222> 51..116
<223> Von Heijne matrix

score 6.5
seq SCLCPALFPGTSS/FI

<221> polyA_signal
<222> 319..324

<221> polyA_site
<222> 339..350

<400> 248
acgtcattcc aaaaccacac ccttgcaaag ctttgtactc cgcaccccag atg atc 56
Met Ile
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20 -15 -10 -5
ggt act tcc tcc ttt att gta gca ctc agc tcc cca gcc gat ctg tac 152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
1 5 10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa 200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
15 20 25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta 242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
30 35 40
tgattttgct gaattttaaa taaaatgaaa accataaatt acatratgct tttattgach 302
cttgacmact ggcctaaata aaaaractct gactccaaaa aaaaaaaa 350

<210> 249
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..191

<221> sig_peptide
<222> 111..155
<223> Von Heijne matrix
score 5.80000019073486
seq FLXLMTLTTHVHS/SA

<221> polyA_signal
<222> 965..970

<221> polyA_site
<222> 986..996

<400> 249
atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct 60
cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy 116
Met Gly
-15
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag 164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
-10 -5 1
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat 211
Pro Asn Glu Gln Pro Trp Leu Leu Asn
5 10
ggtacgcgtt gctatacaga atctttggat atgtgcatca gtggtttatg ccaaattgtt 271

```
ggctgcgatc accagctggg aagcaccgtc aaggaarata actgtggggt ctgcaacrga    331
natgggtcca cctgccggct ggtccgaggg cartataaat cccakctctc cgcaaccaaa    391
tcrgatgata ctgtggttgc aattccctat ggaagtakac atattcgcct tgtcttaaaa    451
ggtcctgatc acttatatct ggaarccawa accctccagg ggactaawgg tgaaaacagt    511
ctcasctcca caggaacttt ccttgtggac aattctagtg tggacttcca gaawtttcca    571
gacwdagaga tactgagaat ggctggacca ctcacagcag atttcattgt caawattcgt    631
aactcgggct ccgctgacag tacagtccag kkcatcttct atcaacccat catccaccga    691
tggagggara cggatttctt tccttgctca gcaacctgtg gaggaggtta tcagctgaca    751
tcggctgagt gctacgatct gaggagcaac cgtgtggttg ctgaccaata ctgtcactat    811
tacccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca    871
gccaggtcag tcaaatttgc tagttcattt gtcataaaca taactcaagt tccaaatagg    931
ttatttaaat taaaatgaaa cgttttaatt aaaaataaaa tgaaattaaa catcaaaaaa    991
aaaaa                                                               996
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<210> 250
<211> 860
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..602

<221> sig_peptide
<222> 45..107
<223> Von Heijne matrix
score 8.5
seq LLTIVGLILPTRG/QT

<221> polyA_signal
<222> 828..833

<221> polyA_site
<222> 850..860

<400> 250

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acctctctcc acgaggctgc cggcttagga cccccagctc cgac atg tcg ccc tct      56
                                                Met Ser Pro Ser
                                                    -20
ggt cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga      104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
        -15                 -10                 -5
gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act      152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
    1               5                  10                  15
atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca      200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
                20                  25                  30
gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca      248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
            35                  40                  45
cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct      296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
        50                  55                  60
cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc      344
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro
    65                  70                  75
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac      392
Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa
80                  85                  90                  95
```

```
gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg      440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg
                100                 105                 110
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt      488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys
            115                 120                 125
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg      536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Ser Pro Val
        130                 135                 140
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag      584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu
    145                 150                 155
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag            632
Ser Ile Arg Asn Arg Ser
160                 165
ccccctgcca gctcaccgtg cccagcctcc tgcatcccct cgaagagcct ggccagagag    692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtctcc tacctccccc    752
aaccctgccc gcccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc    812
tctgctaaga caaaaagtaa agcactgtgg tctttgcaaa aaaaaaaa                860
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<210> 251
<211> 593
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..560

<221> sig_peptide
<222> 24..101
<223> Von Heijne matrix
score 10.3999996185303
seq LLLLLCGPSQDQC/RP

<221> polyA_signal
<222> 563..568

<221> polyA_site
<222> 583..593

<400> 251

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aanccagctg csgccggcca gcc atg gag act gga gcg ctg cgg cgc ccg caa     53
                          Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
                              -25                 -20
ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc      101
Leu Leu Pro Leu Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
    -15                 -10                 -5
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc      149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
1               5                   10                  15
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga      197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly
            20                  25                  30
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag      245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
        35                  40                  45
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac      293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
    50                  55                  60
```

```
aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc      341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65                  70                  75                  80
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac      389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
                85                  90                  95
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg      437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
            100                 105                 110
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan      485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
        115                 120                 125
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa      533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
    130                 135                 140
acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct            580
Thr His Phe Cys Leu Ser Ile Xaa Leu
145                 150
gtaaaaaaaa aaa                                                      593
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<210> 252
<211> 1114
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 109..558

<221> sig_peptide
<222> 109..273
<223> Von Heijne matrix
score 3.70000004768372
seq VAFMLTLPILVCK/VQ

<221> polyA_site
<222> 1104..1114

<400> 252

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attagctstc caaggtctcc cccagcactg aggagctcgc ctgctgccct cttgcgcgcg      60
ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca      117
                                                    Met Ala Thr
                                                    -55
aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga      165
Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
        -50                 -45                 -40
ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc      213
Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
    -35                 -30                 -25
aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc      261
Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
-20                 -15                 -10                 -5
ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act      309
Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
                1                   5                  10
cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc      357
Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
        15                  20                  25
gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc      405
Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe
```

```
   30                  35                  40
ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat      453
Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
45                  50                  55                  60
gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct      501
Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
                65                  70                  75
gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt      549
Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
            80                  85                  90
tat cgc tat tgaatatatt gtcctgacca tgaataggac caacgtcaat             598
Tyr Arg Tyr
        95
gtctttttctg agctttccgc tcctcgtcgc aatgaaaact ttgtcctcct gctcacctac    658
ktcctcttct tgatggcgct gaccttcctc wtgtcctcct tcaccttctg tggtkccttc    718
acgggctgga avagacatgg ggcccacatc tacctcasga tgctcskctc cattgccatc    778
tgggtggcct ggatcaccct gctcatgctt cctgactttg accgcrggtg ggatgacacc    838
atcmtcarct ccgccttggs trcsaatggc tgggtgttcc tgttggctta tgttagtccc    898
gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgctttc    958
tgtaaacctc aactcgtgaa gaagagctat ggtgtgggrga acagagccta skctcaagag   1018
gaaatcactc aaggttttga agagacaggg gacacgctct atgcccccta ttccacacat   1078
tttcagctgc agaascagcc tccccaaaaa aaaaaa                              1114
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<210> 253
<211> 1182
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 128..835

<221> sig_peptide
<222> 128..220
<223> Von Heijne matrix
score 4.69999980926514
seq LAVDSWWLDPGHA/AV

<221> polyA_signal
<222> 1145..1150

<221> polyA_site
<222> 1170..1181

<400> 253

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aagaactgcg tctcgcgacc caggcgcggg ttcccggagg acagccaaca agcgatgctg      60
ccgccgccgt ttcctgattg gttgtgggtg gctacctctt cgttctgatt ggccgctagt     120
gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag gag        169
        Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
            -30                 -25                 -20
gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac       217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
        -15                 -10                 -5
gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt       265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
    1               5                   10                  15
gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg       313
Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro
                20                  25                  30
gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag       361
```

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Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln
          35                  40                  45
gcg tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct      409
Ala Ser Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro
      50                  55                  60
gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc      457
Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala
  65                  70                  75
ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag      505
Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu
80                  85                  90                  95
ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc      553
Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly
              100                 105                 110
cgt agc atc ggg gga wca ccg ccc amc ctg ggt gcc ttg gac ctg ctg      601
Arg Ser Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu
          115                 120                 125
ggc cca gcc act ggc tgt cta ctg gac aat ggg ctt gag ggc ctg ttt      649
Gly Pro Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe
      130                 135                 140
gag gat att gac acc tct atg tat gac aat gaa ctt tgg gca cca gcc      697
Glu Asp Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala
  145                 150                 155
tct gag ggc ctc aaa cca ggc cct gag gat ggg ccg ggc aag gag gaa      745
Ser Glu Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu
160                 165                 170                 175
gct ccg gag ctg gac gag gcc gaa ttg gac tac ctc atg gat gtg ctg      793
Ala Pro Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu
              180                 185                 190
gtg ggc aca cag gca ctg gag cga ccg ccg ggg cca ggg cgc               835
Val Gly Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
          195                 200                 205
tgagccctcg tgctggaatg gttgtctggt atctgaactg agcctgctgg ctggaccaac    895
tgtcctcgaa aagacacagc tggcttccct agtacagaga acagggcttg ggccactttg    955
gagagacaga atctagtcct gggcaacttc acatccgtcc tcctgtctca gggctggcag   1015
ggggagcctg gaattacccc ctagtgatgg aatgacaggg tctggtgggg actgaattcc   1075
ctggccctgg ggtcatagct tgggctgttc cttctctgat acgggaagag acccaatcag   1135
atttttcaaa ttaaagccag tcctgggaaa tctcaaaaaa aaaaaac                 1182
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<210> 254
<211> 1073
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..505

<221> sig_peptide
<222> 59..358
<223> Von Heijne matrix
score 3.70000004768372
seq LASSFLFTMGGLG/FI

<221> polyA_signal
<222> 1042..1047

<221> polyA_site
<222> 1062..1073

<400> 254
actgtttnng ggaggcgcgt ggggcttgag gccgagaacg gcccttgctg ccaccaac 58
atg gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac 106
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100 -95 -90 -85
ctg aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act 154
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70
gtg tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata 202
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55
att tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat 250
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50 -45 -40
gaa cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat 298
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35 -30 -25
gga caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg 346
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20 -15 -10 -5
gga ggt tta ggt ttc ata atc ctg gac gga tcg aat gca cca aat atc 394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
1 5 10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc 442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
15 20 25
cta twr agt ttt tkc ayg gct aga gta ttc atg aga atg aaa ctg ccg 490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
30 35 40
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtggat actggatttg 545
Gly Tyr Leu Met Gly
45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa 605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga 665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttcctgctgg 725
cctattgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata 785
ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat 845
tttttggaga tgacatttct gattttcaga aattaacata aaatccagaa gcaagattcc 905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag 965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcctga acaataagat 1025
gtatgaacgg agcagaaata aatacttttt ctaattaaaa aaaaaaaa 1073

<210> 255
<211> 818
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..207

<221> sig_peptide
<222> 1..147
<223> Von Heijne matrix
score 7.59999990463257
seq HLPFLLLLSCVGX/XP

<221> polyA_signal
<222> 784..789

<221> polyA_site
<222> 807..818

<400> 255
atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat 48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
-45 -40 -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg 96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
-30 -25 -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg 144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Ser Cys Val Gly
-15 -10 -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat 192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
1 5 10 15
ttt ttt att cct gac tgagtcacca cacccctctc ccctgatcaa agggaatatk 247
Phe Phe Ile Pro Asp
20
artttttaat ttggatcgac tgaggtgcca ggagaaactg cagkcccagg tatccmvaca 307
gccaccagga tggtccctcg ccccaccccc accgcctctk ccccaccttt tccaacgtgt 367
tgcatgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga 427
rgtttggarg caaaatcaac ctgggaracc accccggccg cggcgcctca gtggacaggt 487
gggargaaaa gaaaacttct taccttggar garggacatc ccgcttcctt atccttagct 547
tttttgttgc tcctccccac tgccccтttt aatttatttg gttgtttgcg gaaggagggg 607
ggaagggggt aagctgggcc gggaactgtc cgaggtgctg agctggggcg ggaccggaat 667
cctcccggta gggtaccagg gactgagttg ggcctggggc cgtgtccaag gtgccaatga 727
tgcgggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccgga aagaactata 787
aagcgctgga agcgcctgca aaaaaaaaaa a 818

<210> 256
<211> 971
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..734

<221> sig_peptide
<222> 12..101
<223> Von Heijne matrix
score 4.80000019073486
seq ILFCVGAVGACTL/SV

<221> polyA_signal
<222> 914..919

<221> polyA_site
<222> 961..971

<400> 256
aatacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg 50
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
-30 -25 -20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act 98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
-15 -10 -5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag 146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu

```
    1               5                  10                  15
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag      194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
                20                  25                  30
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac      242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn
            35                  40                  45
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg      290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
        50                  55                  60
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act      338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
    65                  70                  75
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg      386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
80                  85                  90                  95
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta      434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val
                100                 105                 110
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct      482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala
            115                 120                 125
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc      530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe
        130                 135                 140
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata      578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile
    145                 150                 155
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa      626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu
160                 165                 170                 175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa      674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln
                180                 185                 190
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac      722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn
            195                 200                 205
tat gaa agg cca tagaaacgtt ttaattttca atgaagtcac tgaaaatcca          774
Tyr Glu Arg Pro
        210
actccaggag ctatggcagt gttaatgaac atatatcatc aggtcttaaa aaaaaataaa    834
ggtaaactga aaagacaact ggctacaaag aaggatgcca raatgtaagg aaactataac    894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa    954
tttgccaaaa aaaaaaw                                                   971
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<210> 257
<211> 640
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 378..518

<221> sig_peptide
<222> 378..467
<223> Von Heijne matrix
score 5.5
seq SLMTCTTLINASA/IS

<221> polyA_signal
<222> 607..612

<221> polyA_site
<222> 628..640

<400> 257
agcctgggta akgcccaaga tggctgtctt cgccttagta ctcgtgtgaa gttggcgggg 60
acggttcctg tcatcttctt gggcttattt ggtgtgctgt tgaaggggg agactagaga 120
aatggcaggg aacctcttat ccggggcagg taggcgcctg tgggactggg tgcctctggc 180
gtgcagaagc ttctctcttg gtgtgcctag attgatcggt ataaggctca ctctcccgcc 240
ccccaaagtg gttgatcgtt ggaacgagaa aagggccatg ttcggagtgt atgacaacat 300
cgggatcctg ggaaactttg aaaagcaccc caaagaactg atcaggggc ccatatggct 360
tcgaggttgg aaaggga atg aat tgc aac gtt gta tcc gaa aga gga aaa 410
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys
-30 -25 -20
tgg ttg gaa gta gaa tgt tcg ctg atg acc tgc aca acc tta ata aac 458
Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn
-15 -10 -5
gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat 506
Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp
1 5 10
aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag 558
Arg Arg Glu Ser
15
ggaaactgta cttttccctg tgaggaaacg gctttgtatt ttctctgtaa taaaatgggg 618
cttctttgga aaaaaaaaaa aa 640

<210> 258
<211> 745
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..304

<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
score 4.59999990463257
seq PLQWSLLVAVVAG/SV

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..743

<400> 258
acttccgcct gcgcctgcgc agcvcagctc cshgagccct gccaaccatg gtgaacttgg 60
gtctgtcccg ggtggacgac gccgtggctg ccaagcaccc ggcaccggc atg gcc ttt 118
Met Ala Phe
ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg 166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
-25 -20 -15 -10
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg 214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
-5 1 5
acg aga gtg gag tcg gag aaa tgc aac aac ctc tgg ctc ttc ctg gag 262

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Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
        10                  15                  20
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc              304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser
    25                  30                  35
taggagagct ccagcagggg cacagargat tgggggcagg argartctgg aacacakcct    364
tcatgccccc tgaccccagg ccgaccctcc ccacacccta gggtacccca gtcgtatcct    424
ctgtccgcat gtgtggccag gcctgacaaa cmcctgcaga tggctgctgc cccaacctgg    484
gacctgccca ggaggttgga gcagaaaggg ctctccctgg ggtggtgttt ctcctctagg    544
gtattgggat gcatgttctg cactgccagc agagagggtg tgtctggggg ccaccaccta    604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc ccctgcatct    664
ccaacaagtc caaggtgaca gctggtgcta ggggcgtggg gttaataaat ggcttatcct    724
tctctccaaa araaaaaaam c                                              745
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<210> 259
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..419

<221> sig_peptide
<222> 201..272
<223> Von Heijne matrix
score 6.40000009536743
seq LSYLPLWLGPIWP/CS

<221> polyA_signal
<222> 601..606

<221> polyA_site
<222> 627..637

<400> 259

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acaaaatata attgcctcts ccctctccca ttttctctct tgggagcaat ggtcacagtc     60
cctggtacct gaaaaggtac ctaggtctag gcccttcttc cctttccctt cctctccccc    120
accccagaac tttggctccc tttcccttct ctctctggta gctccaggag gcctgtgatc    180
cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc    233
                       Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
                                      -20                 -15
ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc      281
Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
            -10                 -5                  1
tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg      329
Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
    5                   10                  15
ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar      377
Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
20                  25                  30                  35
aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg              419
Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
                40                  45
targaaggtc tggcctgggg tcrggtgaag gagggcccag gtcagttctg gggtcccagt    479
gacctgcttt gccattctcc tggtgccgct gctgctccct gtttctggag ctggatgttc    539
cccacctggc agttgagctg cctgagccaa tgtgtctgtc tttggtaact gagtgaacca    599
taataaaggg gaacatttgg ccctgtgaaa aaaaaaaa                            637
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<210> 260
<211> 1315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 123..302

<221> sig_peptide
<222> 123..176
<223> Von Heijne matrix
score 4.30000019073486
seq WTCLKSFPSPTSS/HA

<221> polyA_signal
<222> 1279..1284

<221> polyA_site
<222> 1301..1312

<400> 260
aagagcatcc tgcgccccgg cgcggggccc tgcggtagcc tcaggcccct cccctggacc 60
cgccgcagag ccagtgcaga atacagaaac tgcagccatg accacgcacg tcaccctgga 120
ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167
Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
-15 -10 -5
acc agc agc cat gca tcg agc ctc cac ctt cct cca tca tgt acc agg 215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
1 5 10
cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca 263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
15 20 25
ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat 312
Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
30 35 40
gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgcagct gttcccgggc 372
cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt 432
araggtgctg gagccggagg tcaccaagct catgaagttc atgtattttc arcgcaaggc 492
catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt 552
tgtctctgag gcctacctcc tgacccttgg caagttcatc aacatgtttg ctgtcctgga 612
tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc 672
acagttcctg cggaagatgg cagatcccca gtctatccag gagtcgcaga acctttccat 732
gttcctggcc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc 792
aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa 852
gatgtacctg actcccagtg agaaacatat gctcctcaag gtaaaactcc cctgaggccg 912
cacccatgga gcctgggctt accctctcac cttcttctta ttaaaaatcc gttttaaaaa 972
acaatgtttc ttttttctta aacattgata cagatcttac ggcacataat ggtttgtaac 1032
ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat 1092
ttctacaatg ttatgtgtaa tgactgccaa gtattctgtt gtattggaac attgtcatgt 1152
aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt 1212
tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa 1272
aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc 1315

<210> 261
<211> 1035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..673

<221> sig_peptide
<222> 98..376
<223> Von Heijne matrix
score 5.59999990463257
seq VLLLRQLFAQAEK/WY

<221> polyA_site
<222> 1025..1035

<400> 261
aattttcygt ggtccaacta ccctcggcga tcccaggctt ggcggggcac cgcctggcct 60
ctcccgttcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta 115
Met Ala Glu Leu Gly Leu
-90
aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
-85 -80 -75
tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac 211
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
-70 -65 -60
ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc 259
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
-55 -50 -45 -40
tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa 307
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
-35 -30 -25
tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag 355
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Leu Arg Gln
-20 -15 -10
ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc 403
Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
-5 1 5
tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa 451
Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu
10 15 20 25
aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca 499
Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr
30 35 40
aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta 547
Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Gly Thr Ala Lys Leu Leu
45 50 55
aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg 595
Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu
60 65 70
tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca 643
Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser
75 80 85
ggt cct ctg agg ata att agt cca ttg cag tagttttact tgatggtacc 693
Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
90 95
ccatgggcca gaagagggca tacttaacct tctagagagc ctgaagtagc tcctgatcac 753
acctttttcaa ggtaaagtga agagcatgaa attttggaca gcgtttattg atggacattt 813
aaagtttgtg atctgcggta acaaggagaa gggtttttaa gtttataaaa attatttatc 873
aattagccgg gtgtggtggt acgtgcctat agtcagagct actcgggagg ctgaggcagg 933
agaattgctt gaacccggga ggtggaggtt gcagtgagct gagatcacgc cactgcactc 993
tagcctgggc gacagagcga gactccatct caaaaaaaaa aa 1035

<210> 262
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..463

<221> sig_peptide
<222> 17..232
<223> Von Heijne matrix
score 3.79999995231628
seq LMGLALAVYKCQS/MG

<221> polyA_signal
<222> 657..662

<221> polyA_site
<222> 684..696

<400> 262
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actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act     52
                  Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
                      -70                 -65
atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc     100
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
-60                 -55                 -50                 -45
att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt     148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
                -40                 -35                 -30
tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg     196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
            -25                 -20                 -15
atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta     244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
        -10                 -5                  1
cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga     292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5                   10                  15                  20
atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg     340
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
                25                  30                  35
cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca     388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
            40                  45                  50
gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac     436
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
        55                  60                  65
caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca           483
Gln Lys Thr Leu Phe Ser Met Val Gly
    70                  75
atgtgcatat tacgacaaac acaaaaaaac tataccataa cccagggctg aaaataatgt    543
aaaaaacttt atttttgttt ccagtacaga gcaaaacaac aacaaaaaaa cataactatg    603
taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat    663
taaatggttg araacaatgc aaaaaaaaaa aaa                                696
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<210> 263
<211> 868

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 263..481

<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
score 11.1999998092651
seq ILVVLMGLPLAQA/LD

<221> polyA_site
<222> 858..868

<400> 263
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ccaggcgcgg cggtacctca cggtggtgaa ggtcacaggg ttgcagcact cccagtagac 120
caggagctcc gggaggcagg gccggcccca cgtcctctgc gcaccaccct gagttggatc 180
ctctgtgcgc caccctgag ttggatccag ggctagctgc tgttgacctc cccactccca 240
cgctgccctc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg 292
Met Thr Pro Leu Leu Thr Leu Ile Leu Val
-20 -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt 340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10 -5 1 5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg 388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met
10 15 20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg 436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met
25 30 35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta 481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val
40 45 50
tgatggctac tccaagcacg cgtccaccac ctcctgctgc cagtacgacc tctgcaacgg 541
caccggcctt gccacccccgg ccaccctggc cctggccccc atcctcctgg ccaccctctg 601
gggtctcctc taaagccccc gaggcagacc cactcaagaa caaagctctc gagacacact 661
gctayaccct ckcacccakc tcaccctgcc tcaccctcca cactccctgc gacctcctca 721
gccatgccca gggtcaggac tgtgggcaag aagacacccg acctcccccca accaccacac 781
gacctcactt cgaggccttg acctttcgat gctgtgtggg atcccaaaag tgtccggctt 841
tgatgggctg atcagcaaaa aaaaaaa 868

<210> 264
<211> 775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..299

<221> sig_peptide
<222> 42..101
<223> Von Heijne matrix
score 5.40000009536743
seq WFVHSSALGLVLA/PP

<221> polyA_site

<222> 762..775

<400> 264
aacgatacaa atggtaggcc ttcatgtgag ccagtdacta c atg aat ctt cat ttc 56
Met Asn Leu His Phe
-20
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca 104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro
-15 -10 -5 1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt 152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys
5 10 15
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc 200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr
20 25 30
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa 248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys
35 40 45
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg 296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg
50 55 60 65
cag tgaaactwkk ttcwcttcta aagcccttca tttcccacaa ggttaagctc 349
Gln
tcgaaacccc atttgatcct tggttcctat ttcgatcctc ctttggaatc tgaaaatcgg 409
tctccatgtt gtatgcaaat taaaakttgc cttgtttgtt actcttccaa cacagggtat 469
cagggaraaa gaggccttat ctgttcctcc atccccccctg ttttgacaga ctgctaagaa 529
ttcctcagga cttcctttgg ttggggattt tactttccca aaagtctgat ctgatttctt 589
tcaggggtag acaagcttgt cctagtgctc tgcttcaggt cttatcagaa gaaacccagg 649
aatagaaaag gtagatgcct tgacttttgt ccctgttgtg gggactaaag tgttttttgc 709
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aaaaaa 775

<210> 265
<211> 1075
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..431

<221> sig_peptide
<222> 198..260
<223> Von Heijne matrix
score 6.90000009536743
seq LLACGSLLPGLWQ/HL

<221> polyA_site
<222> 1064..1074

<400> 265
atatatttct gaggcagtac ccatctcact tgtaaactta aaagacaccg cagagatttg 60
agggactcag aagtcaaata gagtaggtta aaaacctctt atttttcaaa ttaattgttt 120
taagaaacaa gcatacctgt gtaagtgaaa tatcttaatt tgtgttgaat caagttagga 180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc 230
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
-20 -15
tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac 278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
-10 -5 1 5

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tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca      326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
          10                  15                  20
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt      374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
      25                  30                  35
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac      422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
  40                  45                  50
tct atc acc tagccattgt akccatacca agccgggctt cctacttccc              471
Ser Ile Thr
55
tctgctcccc ttggtttcct cctgtraart aaatctcact gacccttgat gcasctccaa    531
gcatatataa tatatatata ataaaaccat abtctaaaaa attcaaacca ggawaaataa    591
asccaraaat ttgtatggga aaaatctgca caaatttatt tggccagcat ggttatcatg    651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca    711
actacttacc tctcaatacc aaaaargaag caggaggcaa aatctctcaw taatttcata    771
aaaacaattc ttakctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc    831
saggtgggcg gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc    891
catctctact aaaattacaa aaaattrgct gggcgaggtg gcgggcacct gtggtcccag    951
ctactcggga ggctgaggca agagaatggt gtgaacccca gggggcggag cctgcagtga   1011
gctgagatcg caccactgca ctccagcctg ggcgacagtg agactccgtc tcaaaaaaaa   1071
aaah                                                                1075
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<210> 266
<211> 981
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 279..473

<221> sig_peptide
<222> 279..362
<223> Von Heijne matrix
score 4.40000009536743
seq SCFLVALIIWCYL/RE

<221> polyA_signal
<222> 944..949

<221> polyA_site
<222> 970..981

<400> 266

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agaatcgtgt cttgtgtgcc ccggcggccg ggtgagctcc tcaaggtctc ggagggccga     60
gggcagacac cggcgggcgg gcggasgctt actgctctct ctcttccagg gccgtccggg    120
cgctgaggct cataggctgg gcttcccgaa gccttcatcc gttgcccggt tcccgggatc    180
gggcccaccc tgccgccgag gaagaggacg accctgaccg ccccattgag ttttcctcca    240
gcaaagccaa ccctcaccgc tggtcggtgg gccatacc atg gga aag gga cat cag     296
                                    Met Gly Lys Gly His Gln
                                                    -25
cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
      -20                 -15                 -10
atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
  -5                  1                   5                  10
aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440
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Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu
                15                  20                  25
cct gag act cca gct gcc tac aga gcg aga act tgacggggtg cccgctgggg    493
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
            30                  35
ctggcaggaa gggagccgac asccgccctt cggatttgat ktcacgtttg cccgtgactg    553
tcctggctat gcktgcgtcc tcagcactra argacttggc tggtggatgg ggcacttggc    613
tatgctgatt cgcgtgaagg cggavcaaaa tctcagcaaa tcggaaactg ctcctcscct    673
ggctcttgat ktccaaggat tccatcggca aaacttctca ratccttggg gaaggtttca    733
gttgcactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag    793
cacttctggt gacacttgtc atccagtgtt agtttgcagg taatttgctt tctgagatag    853
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc    913
acatgtgagt tttacacaac aacaaatgaa aataaatttt aattttataa tatgggaaaa    973
aaaaaaaa                                                            981



<210> 267
<211> 1031
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..644

<221> sig_peptide
<222> 12..92
<223> Von Heijne matrix
      score 4
      seq LTFFSGVYGTCIG/AT

<221> polyA_signal
<222> 1002..1007

<221> polyA_site
<222> 1020..1031

<400> 267
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             Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu
                        -25                 -20                 -15
gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca       98
Glu Leu Thr Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr
                    -10                 -5                  1
aat aaa ttt gga gca gaa gag ara agc ctt att gga ctt tct ggc att      146
Asn Lys Phe Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile
        5                   10                  15
ttc atc ggc att gga gaa att tta ggt gga agc ctc ttc ggc ctg ctg      194
Phe Ile Gly Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu
    20                  25                  30
agc aag aac aat cgt ttt ggt aga aat cca gtt gtg ctg ttg ggc atc      242
Ser Lys Asn Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile
35                  40                  45                  50
ctg gtg cac ttc ata gct ttt tat cta ata ttt ctc aac atg cct gga      290
Leu Val His Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly
                55                  60                  65
gat gcc ccg att gct cct gtt aaa gga act gac agc agt gct tac atc      338
Asp Ala Pro Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile
            70                  75                  80
aaa tcc agc aaa raa ttt gcc att ctc tgc akt ttt ctg tkg ggc ctt      386
Lys Ser Ser Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu
```

```
        85                  90                  95
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg      434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu
    100                 105                 110
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag      482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln
115                 120                 125                 130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt      530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu
                135                 140                 145
cac tgg caa ctc ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att      578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile
            150                 155                 160
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc ggc      626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly
        165                 170                 175
tct gac tac cga agt atc tgatctggtg tccgtgaggg gacacgtatg             674
Ser Asp Tyr Arg Ser Ile
    180
acctcagaaa cacagctgga cacagagctt ggtggaagaa gtcgcctttg atcttcacta    734
tatattgggt gatgttcagt atggaaaatc aagggattaa gactgttaaa tcagccagag    794
tkggtgttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt    854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attcttataa    914
tcatgttata gaatgtaaat gttttcttct ctctcctgct cttgttggaa gatcctgcct    974
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```

<210> 268
<211> 1283
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..459

<221> sig_peptide
<222> 91..330
<223> Von Heijne matrix
score 7.69999980926514
seq LVLFLSLALLVTP/TS

<221> polyA_site
<222> 1271..1281

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<400> 268
tattccttgg agttccacga ctgaattaag actgttgtgg grdccataat tttcaaatac     60
ttgccctata ttcgtgttga gggttcacac atg agc aca tgg tat ttg gca ctt      114
                                Met Ser Thr Trp Tyr Leu Ala Leu
                                -80                 -75
aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg      162
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu
        -70                 -65                 -60
tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat      210
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn
    -55                 -50                 -45
tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt      258
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe
-40                 -35                 -30                 -25
ggt ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta      306
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu
```

```
                -20                 -15                 -10
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata      354
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile
            -5                  1                   5
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac      402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp
    10                  15                  20
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt      450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu
25                  30                  35                  40
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct              499
His Gln Leu
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaag    559
ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatttt    619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgctct    679
gttttggaat tgaattagct ttcaggccas cagggcactg tttggtaaat tgctttttcc    739
agtactagca tgttttctcc ctccatagcc tctgttagct tctgagcttg taacctccag    799
ggaaaavatga gaatattcac ccttttaata tgtgtagaga ccatgcaaga ccattgtctt    859
ctaataatta gaaatactta gccagattct ctatagtaaa cccggagatt gggagggctg    919
ctttctactt ggtgcatcct tctgcgcttc taatgatttt taaaaatctg ttaataattg    979
atgttttctg gctgggcaca gtggctcacg cctgtaatcc cagcactttg ggaggccaag   1039
gagggcagat catgaggtca ggagattgar accatcctgg ctaacacggt gaaaccccgt   1099
ctctactaaa aatacaaaar aattakccgg gcatggtagt gggcgcctgt gtacccagct   1159
actggggagg ctgaggcarg araatcgctt gaacctggga ggcggaggtt gcastragct   1219
gagatggtgc caccgcactc tagcctgggt gacagagcga gacttcattt caaaaaaaaa   1279
aamc                                                               1283
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<210> 269
<211> 1777
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..327

<221> sig_peptide
<222> 70..147
<223> Von Heijne matrix
score 9.60000038146973
seq WLIALASWSWALC/RI

<221> polyA_signal
<222> 1741..1746

<221> polyA_site
<222> 1763..1774

<400> 269

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agcccggttt cgtgcccgcg gccgactgcg casctgtccg cgagtctgag atacttacag      60
agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg     111
          Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
              -25                 -20                 -15
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt      159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
        -10                 -5                  1
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt      207
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu
5                   10                  15                  20
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat      255
```

```
Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp
                25                  30                  35
gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat      303
Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp
            40                  45                  50
tcc cat gcc cac tgg cmt tcg rca taaaaaaatt ttcatcagaa ccaaagatgg     357
Ser His Ala His Trp Xaa Ser Xaa
        55                  60
aatacgtctg aatcttattt tgatacgata cactggagac aattcaccct attccccaac    417
tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac    477
ttatgttggt taacctcaaa gttaaccttt tgctggttga ttatcgagga tatggaaaaa    537
gtgaaggaga agcaagtgaa gaaggactct acttagattc tgaagctgtg ttagactacg    597
tgatgactag acctgacctt gataaaacaa aaatttttct ttttggccgt tccttgggtg    657
garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatggtgg    717
agaacacatt tttaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc    777
gttaccttcc tttatggtgc tacaaaaata aatttttgtc ctacagaaaa atctctcagt    837
gtagaatgcc ttcacttttc atctctggac tctcagatca attaattcca ccagtaatga    897
tgaaacaact ttatgaactc tccccatctc ggactaagan attagccatt tttccagatg    957
ggactcacaa tgacacatgg cagtgccaag gctatttcac tgcacttgaa cagttcatca   1017
aagaagtcgt aaagagccat tctcctgaag aaatggcaaa aacttcatct aatgtaacaa   1077
ttatataatg tttccctttt tgattattgc attgtatttt aatttgtgca gaatgataaa   1137
gaatgttcct tttagaagtg tgttatgtct gtacctgtct gaagagtgac attaaacttt   1197
gaaaggactt cactgctcct ttacgatatt ccaaatagtt ttttacattg gaaaaactaa   1257
ttcttgggat tctttcatac attttcatca aaactttcag tgtgattatg tattcatatc   1317
ttcagtttaa tatgtcagta taatagatat tgttcaaaag tttcttgttg ctaaagtggt   1377
gtaatctgtt acacagatga atagctagat gtggaaagag atatgtaaac aagaaacctt   1437
tgggtattgt ttcttaagta aatattggga caatcatggt aagcaaactt agttctgtaa   1497
ctgcattttt caccttaaaa gttaaatgaa atgcatgatg gtattttatt ccttgaatta   1557
tgcaatgcaa cattttacat gtaaatagca ctggtcatat actgatgtat atggttatct   1617
gggttatatc tatttttatg taaactctat ttttgttttt ggcaagaagt gaaattgaga   1677
cttatgtgca ggttgccatt gaattttgct ctggtgaatg ctgagatcca gctttttctt   1737
acaaataaat gggaccctgt tttccaaaaa aaaaaaamcm                         1777
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<210> 270
<211> 970
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..497

<221> sig_peptide
<222> 12..104
<223> Von Heijne matrix
score 5.5
seq LVGVLWFVSVTTG/PW

<221> polyA_signal
<222> 935..940

<221> polyA_site
<222> 955..967

<400> 270
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aggtctccaa g atg gcg gcc gcc tgg ccg tct ggt ccg kct gct ccg gag      50
              Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
                  -30                 -25                 -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
```

```
            -15                 -10                 -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
        1               5                   10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
15                  20                  25                  30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
                35                  40                  45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
            50                  55                  60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
        65                  70                  75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
    80                  85                  90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
95                  100                 105                 110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
                115                 120                 125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
            130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact    597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt    657
gagcctcctt gattttaata gagaacttct agtgtatgga tttaaagatt tctctttttc    717
attcatatac cattttatga gttctgtata atttttttgtg gtttttgttt tgttgagtta    777
aagtatatta ttgtgagatt tatttaatag gacttccttt gaaagctgta taatagtgtt    837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac    897
aaaggcaagt tgccacttgt catttttgtt tctgaaaaat aaaagtataa cttattcaca    957
aaaaaaaaaa mms                                                      970


<210> 271
<211> 645
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..383

<221> sig_peptide
<222> 90..200
<223> Von Heijne matrix
      score 4.90000009536743
      seq MLIMLGIFFNVHS/AV

<221> polyA_signal
<222> 609..614

<221> polyA_site
<222> 632..643

<400> 271
atctctgccc ccctgcgagg gcatcctggg ctttctccca ccgctttccg agcccgcttg     60
```

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cacctcggcg atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg      113
                                Met Ala Ser Leu Leu Cys Cys Gly
                                    -35                 -30
ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc      161
Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
            -25                 -20                 -15
atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg      209
Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
        -10                 -5                  1
att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car      257
Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln
    5                   10                  15
aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct      305
Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala
20                  25                  30                  35
gca ggc ctt tac ctc ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg      353
Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Xaa Arg
                40                  45                  50
ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccg gcgcgtttcc        403
Leu Asn Lys Arg Lys Glu Tyr Met Val Arg
            55                  60
ccgctccagc ccctcctcta tttaaaract ccctgcaccg tktcacccag gtcgcgtccc    463
acccttgccg gcgcccctctg tgggactggg tttcccgggc rararactga atcccttctc    523
ccatctctgg catccggccc ccgtggarar ggctgaggct ggggggctgt tccgtctctc    583
cacccttcgc tgtgtcccgt atctcaataa agagaatctg ctctcttcaa aaaaaaaaaa    643
my                                                                   645
```

<210> 272
<211> 773
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 332..541

<221> sig_peptide
<222> 332..376
<223> Von Heijne matrix
score 3.59999990463257
seq FLPCCLLWSVFNP/ES

<221> polyA_signal
<222> 739..744

<221> polyA_site
<222> 761..773

<400> 272

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aaaacaattc atgcctttca tagtttatta ttattaaagt ctaaacaaaa ttgcaatttc      60
ttaggtaacc ttatatttac aataaatgaa gattaccctc aaatgctaga agctgtctag     120
gtccgtccgg tgtgtcagat tttcctcaga ttagatgtgc caataaccaa gtttattcag     180
taaacaactt gtacttgttt catctggttt tattactctc acccataaac agtaatgact     240
ctctgaccct ctggaaatat gtaatgcttc caatcttgct ttgtgtatct catttaattt     300
gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt        352
                                  Met Arg Phe Leu Pro Cys Cys
                                  -15                 -10
ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt      400
Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe
        -5                  1                   5
```

```
ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca      448
Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser
    10                  15                  20
ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac      496
Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
25                  30                  35                  40
ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act           541
Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
                45                  50                  55
tgaaaagaaa gtgttttatt ttcaaatctg gtccatattt acattctagt tcagagccaa    601
gccttaaact gtacagaatt tccactgtaa ttaaaactat ttagtgttag ttataaatag    661
ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggtgaatgt    721
atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa             773
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<210> 273
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 43..222

<221> sig_peptide
<222> 43..177
<223> Von Heijne matrix
score 4
seq ENFLSLLSKSCSA/DP

<221> polyA_signal
<222> 530..535

<221> polyA_site
<222> 555..566

<400> 273

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aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt        54
                                               Met His Ser Leu
                                               -45
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg      102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg
    -40                 -35                 -30
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt      150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu
-25                 -20                 -15                 -10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc      198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
                -5                  1                   5
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc     252
Met Arg Asp Ile Glu Thr Asn Lys
        10                  15
tacaaaaaga araccagtct atcctgctgg agacagtggc cacgtgaara aagagctctt    312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcatcttggt    372
ttcggacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat    432
ctaactacat gagtgagacc agttgacaac acatggagca racatgagct gttctcagtg    492
artcctacac aaattcctga ctcacaacac tgtgagcaat aaaatggttg ttattttaag    552
ccaaaaaaaa aaaa                                                      566
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<210> 274
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..231

<221> sig_peptide
<222> 115..180
<223> Von Heijne matrix
score 5
seq HLFVTWSSQRALS/HP

<221> polyA_signal
<222> 419..424

<221> polyA_site
<222> 445..455

<400> 274
aacctgccag tkatgcaaat gccaaaatgt gggtcatcat atagtatatt tgaaaccttt 60
ctgaacatgt acaccaccca atgctagagg ctgacttgga aaccggtggg tgca atg 117
Met
ccc gag gct gtg gaa caa tca gcc cat ctc ttt gtg acc tgg agc agt 165
Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser Ser
-20 -15 -10
cag agg gcc ctc agt cac ccc gcc cca ttc ctc acc ara raa aar aat 213
Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys Asn
-5 1 5 10
cca ttt cta tgg aag ctc tgacgtaact tcagtgtttt ctacaatact 261
Pro Phe Leu Trp Lys Leu
15
cctcctgccc cgccccatta aaacagttct tttgttaaaa aatavcctaa tggtccaact 321
ttgctgtctg ttcttccaaa tgtttataat acacattatt tataaatatg tctgtttggg 381
aagctaagaa caagctagtt tttacaacac aaatggaaat aaatgcaatt attataaaaa 441
tycaaaaaaa aaaa 455

<210> 275
<211> 673
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..384

<221> sig_peptide
<222> 232..300
<223> Von Heijne matrix
score 3.70000004768372
seq FFLCAAFPLGAGV/KM

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 662..673

<400> 275
atttggcttg cagactgcct tctatcccag aacagctgag aaatctatga agctgagatt 60
ctgaaggacc cagcttaggt tcttccactt aggcctcaat tcccttcctt ttccaggggc 120
agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttcctttc ccagaagcca 180
ctggcccccc atagcaccca gtgcatcctt tttacaagtg gaagaactag g atg gct 237
Met Ala
ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc 285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
-20 -15 -10
ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca 333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
-5 1 5 10
ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg 381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
15 20 25
cct tagcttctgg gcctatcsgc tgccttccct cttyttccta ccacctcttc 434
Pro
tgccttcctt trawctctgt tgggcttggg gatcttagtt ttcttttgtt tatttcccat 494
ctcatttttt tcttctggtc agttttttta agggggggtg ttgtggtttt ttgtttttgt 554
tttgcttctg aaaaarcatt tgcctttctt cctctcccaa cataacaatc gtggtaacag 614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa 673

<210> 276
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..427

<221> sig_peptide
<222> 143..286
<223> Von Heijne matrix
score 7.5
seq FVILLLFIFTVVS/LV

<221> polyA_signal
<222> 606..611

<221> polyA_site
<222> 628..639

<400> 276
aatcgcttca gcagcatcct ctcagacaag agccactatt tctgattcag atcacctgtc 60
atcgaagttt aaagaagggg aaacaggaga cagaaataca ctgaaccaaa aagattcaaa 120
agagcaagtg gaatctctaa ga atg gct tcc agc cac tgg aat gaa acc act 172
Met Ala Ser Ser His Trp Asn Glu Thr Thr
-45 -40
acc tct gtt tat cag tac ctt ggt ttt caa gtt caa aaa att tac cct 220
Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro
-35 -30 -25
ttc cat gac aac tgg aac act gcc tgc ttt gtc atc ctg ctt tta ttt 268
Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile Leu Leu Leu Phe
-20 -15 -10
ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc ctt tat gaa gtg 316
Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe Leu Tyr Glu Val
-5 1 5 10
ctt gam wgc tgc tgc tgt gta aaa aac aaa acc gtg aaa gac ttg aaa 364
Leu Xaa Xaa Cys Cys Cys Val Lys Asn Lys Thr Val Lys Asp Leu Lys

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                15                  20                  25
agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt      412
Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg
            30                  35                  40
gaa act gaa gtg gtc taacactcta taraaaatga acaaaatctc tgaaagcagc      467
Glu Thr Glu Val Val
        45
tcaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc    527
tgactgaatg gttaaaacat ttctagtara aggggaaaaa aaakttaaac atgcactgtt    587
tgtgtgtata sccatttcat taaatataca gtaaaactyc aaaaaaaaaa aa            639
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<210> 277
<211> 772
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 284..463

<221> sig_peptide
<222> 284..379
<223> Von Heijne matrix
score 3.79999995231628
seq TFINITLWLGSLC/QR

<221> polyA_site
<222> 762..772

<400> 277

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acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcgc     60
cctgtattgc acttttggtt ttaaggactg gacccagagt tcctgaaagc caaactccat    120
aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct    180
gttgaatgaa ggtagacgca gcaggcagtt tgtccttacc agtgacctgg aagacggtgg    240
cacttcctga gtgagctcac ttaccttccc tgaatggtga ggc atg gat gaa tat      295
                                              Met Asp Glu Tyr
                                                  -30
tcc tgg tgg tgc cac gtg tta gag gtg gta aag ggt caa atg ttt act      343
Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr
            -25                 -20                 -15
ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc      391
Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe
        -10                 -5                  1
tat gcc tcg ggt act tat ttc cta ata tat atc agc aca gta acg cct      439
Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro
5                   10                  15                  20
agc tgg agg ctt tgt ctt gtt agt tgataaatta gtggtaacag gtagatttgg     493
Ser Trp Arg Leu Cys Leu Val Ser
                25
ttacctccca aagtgctggg attrcagacg tgagccaccg cgcctggccg aaacaattct    553
tttgaaagag agaagtctcc ctgtgttgcg caggctggtc tcagactcct ggggtcaagt    613
gagcctcctg ctttcgcctc ctaaagtgct gggattacag gcgtgagcca ccgcacccgg    673
acagatgtgt tgattttaaa gtgggtatga ggcctgagcc ctggagtttg agaccagcct    733
ggacaacatg gcaagaccct gtctctccaa aaaaaaaaa                           772
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<210> 278
<211> 840
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 162..671

<221> sig_peptide
<222> 162..398
<223> Von Heijne matrix
score 4.09999990463257
seq QGVLFICFTCARS/FP

<221> polyA_signal
<222> 805..810

<221> polyA_site
<222> 830..840

<400> 278
aaaaactgag gcctgggagc aggaacctgt aggcagcgct tgagggtagc gggatagcag 60
ctgcaacgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120
atgtttcccg ggaagaactg ggataaaggg gtcccagcac c atg gag gac ccg aac 176
Met Glu Asp Pro Asn
-75
cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc 224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
-70 -65 -60
cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc 272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
-55 -50 -45
cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg 320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met
-40 -35 -30
aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc 368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
-25 -20 -15
ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc 416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala
-10 -5 1 5
ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg 464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu
10 15 20
ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt 512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
25 30 35
ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr 560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa Arg His Xaa Gln Xaa
40 45 50
cat gar gtc cgt gcc cct cct ggc acc ttc gcc tgc aca rad tgc ggt 608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Xaa Cys Gly
55 60 65 70
cag gac ttt gct car gaa rca ggg ctg cat caa cac tac att cgg cat 656
Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln His Tyr Ile Arg His
75 80 85
gcc cgg ggg gga ctc tgagttcagc ttaagcctct ccacggtgac gggtggctct 711
Ala Arg Gly Gly Leu
90
gtggctggta ggactcaccc atgatatggg gtgcaggaac tctgggggcc ctgaaggatt 771
tgcttccctc ccctgggaag gcagagggct cttaataaag aggacccaka agattcttaa 831
aaaaaaaaa 840

<210> 279
<211> 840
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..632

<221> sig_peptide
<222> 63..308
<223> Von Heijne matrix
score 4.40000009536743
seq NLPHLQVVGLTWG/HI

<221> polyA_signal
<222> 808..813

<221> polyA_site
<222> 829..840

<400> 279
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ga atg tat gtd tgg ccc tgt gct gtg gtc ctg gcc cag tac ctt tgg 107
Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp
-80 -75 -70
ttt cac aga aga tct ctg cca ggc aag gcc atc tta gag att gga gct 155
Phe His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala
-65 -60 -55
gga gtg agc ctt cca gga att ttg gct gcc aaa tgt ggt gca gaa gta 203
Gly Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val
-50 -45 -40
ata ctg tca gac agc tca gaa ctg cct cac tgt ctg gaa gtc tgt cgg 251
Ile Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg
-35 -30 -25 -20
caa agc tgc caa atg aat aac ctg cca cat ctg cag gtg gta gga cta 299
Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu
-15 -10 -5
aca tgg ggt cat ata tct tgg gat ctt ctg gct cta cca cca caa gat 347
Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp
1 5 10
att atc ctt gca tct gat gtg ttc ttt gaa cca gaa rat ttt gaa gac 395
Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp
15 20 25
att ttg gct aca ata tat ttt ttg atg cac aar aat ccc aag gtc caa 443
Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln
30 35 40 45
ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct 491
Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala
50 55 60
tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct 539
Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser
65 70 75
ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga 587
Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg
80 85 90
cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc 632
His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
95 100 105
tgaattatac ctacaacctg ttctgggaca gtatcaatac tgatgagcaa cctggcacac 692
aaactatgag cagaccactt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg 752

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tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa    812
aatacgtatt acaagcaaaa aaaaaaaa                                       840
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<210> 280
<211> 849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..362

<221> sig_peptide
<222> 21..200
<223> Von Heijne matrix
score 4.80000019073486
seq LVILSLKSQTLDA/ET

<221> polyA_signal
<222> 821..826

<221> polyA_site
<222> 838..849

<400> 280

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                      Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
                      -60                 -55                 -50
tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca      101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
                  -45                 -40                 -35
gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att      149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
              -30                 -25                 -20
aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat      197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
          -15                 -10                 -5
gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga      245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
    1               5                   10                  15
atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt      293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
                20                  25                  30
tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg      341
Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu
            35                  40                  45
ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt         392
Phe Glu Leu Phe Ser Ser Lys
        50
ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga ttkctctakg ctygckgttg    452
gaatataacc aattataccw cagctgtaka aatwttgttt taatgtgggg taccyggtgt    512
ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt    572
catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga    632
gcttaaagca agtcttcact tgaaaactgc tatagaaatg ctttatattt aaaaatgaaa    692
gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc    752
tctgtgcttc ttctgccata ccttgcccta tgcatctctt tgtttcaatc ctttgtcata    812
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<210> 281
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..503

<221> sig_peptide
<222> 21..344
<223> Von Heijne matrix
score 5.30000019073486
seq ACMTLTASPGVFP/SL

<221> polyA_signal
<222> 1305..1310

<221> polyA_site
<222> 1330..1341

<400> 281
aaacaactcc ggaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag 53
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-105 -100
tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca 101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
-95 -90 -85
atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc 149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
-80 -75 -70
aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt 197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
-65 -60 -55 -50
tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct 245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
-45 -40 -35
aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag 293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
-30 -25 -20
gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc 341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
-15 -10 -5
ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg 389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
1 5 10 15
cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa 437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
20 25 30
aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg 485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
35 40 45
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag 533
Glu Lys Ser Ile Met Leu
50
atgatgaccg ttcattaata aatttgcatc tcatgcacac cagttacttc ctctttgtga 593
tggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga 653
gcaatcctga attttgtccc gagaaggtgg ctttggctga agcctaattc cacagctcct 713
tgtttttga gagagactga gagaaccata atccttgcct gctgaaccca gcctgggcct 773
ggatgctctg tgaatacatt atcttgcgat gttgggttat tccagccaaa gacatttcaa 833
gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg 893
cacgtgcttt gccctgggta cagccagagc ccttcaaccc caccttggac ttgaggacct 953

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acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac   1013
gatgttttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttggtttgg   1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacctt tgatacggta   1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg cttaataatc   1193
atagtaacaa caataatacc ttttttctcca ttttgcttgc aggaaacata ccttaagttt   1253
tttttgtttt gtttttgttt ttttgttttt tgttttcctt tatgaagaaa aaataaaata   1313
gtcacatttt aatacyaaaa aaaaaaaamc h                                  1344
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<210> 282
<211> 671
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..201

<221> sig_peptide
<222> 1..63
<223> Von Heijne matrix
score 5.09999990463257
seq LLLKIWLLQRPES/QE

<221> polyA_signal
<222> 637..642

<221> polyA_site
<222> 660..671

<400> 282

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atg ctg gga ggt gac cat agg gct ctg ctt tta aag ata tgg ctg ctt      48
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
    -20                 -15                 -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg      96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
-5                  1                   5                   10
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt     144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
            15                  20                  25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca     192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
        30                  35                  40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg             241
Leu Arg Met
    45
ctcagttcat ttaaaaaaga tatctatttg aaagttctca rarttgtaca tatgtttcac   301
agtacaggat ctgtacataa aagtttcttt cctaaaccat tcaccaagag ccaatatcta   361
ggcatttttct tggtagcaca aatttttctta ttgcttaraa aattgtcctc cttgttattt  421
ctgtttgtaa racttaagtg agttaggtct ttaaggaaag caacgctcct ctgaaatgct   481
tgtctttttt ctgttgccga aatarctggt ccttttttcgg gagttaratg tatarartgt   541
ttgtatgtaa acatttcttg taggcatcac catgaacaaa gatatatttt ctatttattt   601
attatatgtg cacttcaaga agtcactgtc agagaaataa agaattgtct taaatgtcaa   661
aaaaaaaaaa                                                          671
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<210> 283
<211> 1601
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..1034

<221> sig_peptide
<222> 39..134
<223> Von Heijne matrix
score 6.09999990463257
seq LPLLTSALHGLQQ/QH

<221> polyA_signal
<222> 1566..1571

<221> polyA_site
<222> 1587..1597

<400> 283
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Met Ile Xaa Leu Arg Asp
-30
aca gct gcc tcc ctc cgc ctt gag aga gac aca agg cag ttg cca ctg 104
Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
-25 -20 -15
ctc acc agt gcc ctg cac gga ctg cag cag cag cac cca gcc ttc tct 152
Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser
-10 -5 1 5
ggt gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt 200
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
10 15 20
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc 248
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Ala Leu Phe
25 30 35
ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc 296
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
40 45 50
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc 344
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
55 60 65 70
ctc ttt gtc aac ctc aat aat gag ctc act gtg gag gag cag gtg gar 392
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
75 80 85
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc 440
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
90 95 100
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga 488
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
105 110 115
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc 536
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
120 125 130
ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac 584
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
135 140 145 150
atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att 632
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
155 160 165
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr 680
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser
170 175 180
cca gct gcc tcc ttc tgc cgg ggc ctg ctc agc cag ccg ggg ccc tca 728
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser

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        185                 190                 195
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg      776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr
    200                 205                 210
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc ttc tat gac cag      824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln
215                 220                 225                 230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag      872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln
                235                 240                 245
ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct      920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser
            250                 255                 260
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag      968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu
        265                 270                 275
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga     1016
Asp Phe Ala Val Leu Gly Glu Gly Leu Val Gln Thr Val Glu Ala Arg
    280                 285                 290
agt gag agg tgg act gtg tgatcccagc tctggagcaa gctgtagacg            1064
Ser Glu Arg Trp Thr Val
295                 300
gacagcagga cattggacct ctagagcaag atgtcagtag gatgacctcc accctccttg   1124
gacatgaatc ctccatggag ggcctgctgg ctgaacatgc tgaatcatct ccaacaaaac   1184
ccagccccaa ctttctctct gatgctccag cattggggca ggggcatggt ggcccatgta   1244
gtctcctggg cctcaccatc ccagaagagg agtgggagcc agctcagaga aggaactgaa   1304
cccaggagat ccatccacct attagccctg ggcctggacc tccctgcgat ttcccactcc   1364
tttcttagtc ttcttccaga aacagagaag gggatgtgtg cctgggagag gctctgtctc   1424
cttcctgctg ccaggacctg tgcctagact tagcatgccc ttcactgcag tgtcaggcct   1484
ttagatggga cccagcgaaa atgtggccct tctgagtcac atcaccgaca ctgagcagtg   1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gcaaaaaaaa aaamcch      1601
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<210> 284
<211> 1206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..263

<221> sig_peptide
<222> 69..125
<223> Von Heijne matrix
score 3.90000009536743
seq ALSMSSFSFHSSS/CS

<221> polyA_signal
<222> 1173..1178

<221> polyA_site
<222> 1196..1205

<400> 284

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acatttgtga ctttaccaat accctcccag ttcttgatag acagctgtag gttgctgggt     60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt     110
         Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
                        -15                 -10
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc     158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser
```

```
-5                  1                   5                  10
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
            15                  20                  25
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys
        30                  35                  40
att gtg ggc tgatttggtc ttcctctcct cctcccactg ttactgccct              303
Ile Val Gly
    45
gcagcccttg ttcaggtgta cagaccctta ttctggcctc tagtgtcctt gtctgtcatg    363
acacaccctt ccgcccaaat acctctgacc ccaaggctgg aatggggctg gtaggarata    423
agtttgctta ctcatartca tgtccttttct cttggcacct gcttccctgc ggtgtcctca    483
aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt    543
gtattattat taagggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa    603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt    663
cctgaggcag tggctgccac ccctttтcar atgtttagtc ctgcaaatag catctttctt-   723
gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat    783
caakttgagt ttttttccag caggggttar gggaggtact csctgttgat atttgacact    843
araaagtaat ctttttтaca aaactgtttt tctaggtggg tggaaagtga aactgccaca    903
tccttgttgg tttagtccaa raratcattt gcaacaacag taratgtccg ggttttgttt    963
ctgtcttttt attatgaaaa actatgttaa gggggaaaat gtggattatg gtaaccarag   1023
gaatccctas ccttgttttc cttaraarac ttgtttagtg ttttatcara cgtctgttgt   1083
agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgtttttgca   1143
caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gttttaccat ttaaaaaaaa   1203
aat                                                                1206
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<210> 285
<211> 536
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..285

<221> sig_peptide
<222> 115..204
<223> Von Heijne matrix
score 3.70000004768372
seq SMMLLTVYGGYLC/SV

<221> polyA_signal
<222> 505..510

<221> polyA_site
<222> 525..536

<400> 285

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acgagtgctg cgttcggctg tgctgggaag ttgcgtagac agtggcctcg agaccctgcc     60
tgcctgagga ggcctcggtt ggatgcgaag gagctgcagc atccagggga caag atg       117
                                                            Met
                                                            -30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc       165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
                -25                 -20                 -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga       213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
            -10                 -5                  1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa       261
```

```
Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
    5                  10                  15
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcctgagcar     315
Glu Gln Lys Xaa Ser Gly Ile Met
20                  25
asakgcccaa ggcatgctgt ggagagactt cacctgccac catttccagg tcaacaggac     375
tagagcgttg atggttttca aaccctgttg gaagaaagtg cccatggttt ctctggttct     435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca     495
cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a                         536



<210> 286
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..344

<221> sig_peptide
<222> 90..140
<223> Von Heijne matrix
      score 8.19999980926514
      seq LLLITAILAVAVG/FP

<221> polyA_signal
<222> 500..505

<221> polyA_site
<222> 515..527

<400> 286
aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca      60
gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc       113
                               Met Lys Lys Val Leu Leu Leu Ile
                                   -15                 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag       161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                -5                  1               5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr       209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
        10                  15                  20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att       257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
    25                  30                  35
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata       305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile
40                  45                  50                  55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa        354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                60                  65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat     414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta     474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc          529



<210> 287
<211> 493
<212> DNA
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<213> Homo sapiens

<220>
<221> CDS
<222> 57..311

<221> sig_peptide
<222> 57..107
<223> Von Heijne matrix
score 8.19999980926514
seq LLLITAILAVAVG/FP

<221> polyA_signal
<222> 467..472

<221> polyA_site
<222> 482..493

<400> 287
aacttgccat ttctcataac agcgtcagag agaaagaact gactgaaacg tttgag atg 59
Met
aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt 107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
-15 -10 -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac 155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
1 5 10 15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca 203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
20 25 30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga 251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
35 40 45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt 299
Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
50 55 60
ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga 351
Pro Ser Glu Lys
65
aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaa gaaaaacaaa 411
tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa 471
acatgaaagc aaaaaaaaaa aa 493

<210> 288
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..302

<221> sig_peptide
<222> 96..182
<223> Von Heijne matrix
score 5
seq ELSLLPSSLWVLA/TS

<221> polyA_site
<222> 501..514

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<400> 288
aagagacgtc accggctgcg cccttcagta tcgcggacgg aagatggcgt ccgccacccg      60
tctcatccag cggctgcgga actgggcgtc cgggc atg acc tgc agg gga agc         113
                                        Met Thr Cys Arg Gly Ser
                                                            -25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca         161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
            -20                 -15                 -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca         209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
        -5                  1               5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt         257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10                  15                  20                  25
crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg             302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
                30                  35                  40
tagctgccac tgaaaaraag gcggtgactc cagctcctcc cataaagagg tgggagctgt      362
cctcggacca gccttacctg tgacactgca ccctcacggc cacccgacta ctttgcctcc      422
ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gctcaggtat      482
cacttctagt tttactttaa aaaataaaaa aatagagac                             521


<210> 289
<211> 811
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..526

<221> sig_peptide
<222> 161..328
<223> Von Heijne matrix
      score 4.19999980926514
      seq XSPLLTLALLGQC/SL

<221> polyA_site
<222> 799..811

<400> 289
aaaaaattgc agtgctgaag acactggacc cgcaaaaggc tgtccctccc aaacctggga      60
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagtac      120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc         175
                                        Met Val Pro Trp Pro
                                            -55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc         223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
    -50                 -45                 -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct         271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35                 -30                 -25                 -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg         319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
                -15                 -10                 -5
ggt cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa         367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
            1               5                   10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg         415
```

```
Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
    15                  20                  25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa      463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
30                  35                  40                  45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt      511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
                50                  55                  60
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaas ccttcaaara      566
Gln Phe Phe Leu Gly
            65
caatgttatt acagcaktct ccccttatcc aaaktttcct tttcctgadt ttcagttagc    626
tatggtcaac cgcttggaaa atakttgaac acagtacaat aaratatttt gaggctggga    686
ktggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact    746
tgaacccagg aktttgarac cascctgggc aacatrgtra gacctcatct ctacaaaaaa    806
aaaaa                                                               811
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<210> 290
<211> 625
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..332

<221> sig_peptide
<222> 210..299
<223> Von Heijne matrix
score 8.10000038146973
seq ITCLLAFWVPASC/IQ

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 613..625

<400> 290

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acaggtcsmc ttaacatctc ttgatttgag ccactcccac tgtcatcagc tttcacctgg     60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccctaaaa    120
atgcattgca tagttgatca agtcactctc tggcctaaaa ccttccttgg ctccctgctg    180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc      233
                              Met Ala Cys Glu Thr His Gly Val
                              -30                 -25
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc      281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
        -20                 -15                 -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca      329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
    -5                  1                   5                   10
ctc tgattcctcc tttcttttgg tcacagagaa agggtacttt ctctgtcaaa           382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc    442
accctggcat actacacara tcactctggg ctcacttgcc tgcctaatgg tcatctcccc    502
agtaaactgt aagctccttg agggcaagga ttgtgttgga atttttgtat taacagtgcc    562
tggcttggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa    622
aaa                                                                 625
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<210> 291
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..361

<221> sig_peptide
<222> 212..319
<223> Von Heijne matrix
score 4.09999990463257
seq HWLFLASLSGIKT/YQ

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 673..684

<400> 291
atccccawns cactctctca cagagactgt tcttttcctt ctgagaccct actccagctt 60
gtagttctaa atctgtgatt atgcactgtc tgtcttcctc ttgaggtcag gggccatttc 120
ttttgttctc tgctatgctc aggacccaga tcaaaggagc tcagtaacta tttacaggcg 180
tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc 232
Met Ala Pro His Thr Ala Ser
-35 -30
ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag 280
Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
-25 -20 -15
cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc 328
His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
-10 -5 1
tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra 381
Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile
5 10
aggtgttaat ggtggtaatg gcataktatt tattacccca ggggacccak aacggtggta 441
tcaaaacata tcattcccca gtggtttaaa actctggtag ctttccargg aatccaaagt 501
ggaatccagt ctccttagct gawttcacag ggccccgtct gcacaacttg gcttctgtcg 561
gcttccctan ccctgacttc ccaagcctta gtcatcaccc tctctcccac ccagggctca 621
gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcat yaaaaaaaaa 681
aaa 684

<210> 292
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 75..482

<221> sig_peptide
<222> 75..128
<223> Von Heijne matrix
score 3.59999990463257
seq KMLISVAMLGAXA/GV

<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

<400> 292
aagtgagacc gcgcggcaac agcttgcggc tgcggggagc tcccgtgggc gctccgctgg 60
ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
-15 -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg 158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
-5 1 5 10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg 206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
15 20 25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg 254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
30 35 40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg 302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
45 50 55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac 350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
60 65 70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc 398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
75 80 85 90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg 446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
95 100 105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg 492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
110 115
tcgggtgagc acgtgtcccc caaaccctgg actgactgct ttaaggtccg caaggcgggc 552
cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc 612
cammcaaaaa aaaaah 628

<210> 293
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..631

<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
score 8
seq LTLIGCLVTGVES/KI

<221> polyA_signal
<222> 777..782

<221> polyA_site
<222> 801..812

```
<400> 293
aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                                    Met Gln Asp
                                                    -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
        -60                 -55                 -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
    -45                 -40                 -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
-30                 -25                 -20                 -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
                -10                 -5                  1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
        5                   10                  15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
    20                  25                  30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
35                  40                  45                  50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
                55                  60                  65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
            70                  75                  80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
        85                  90                  95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
    100                 105                 110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc          631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
115                 120                 125
taaactggaa ctggacccag gatgctttgc ascaacgccc tagggtttgc agtgaatgtc    691
caaatgcctg tgtcatcttg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg    751
gaaaattaag ctatactttt aagaaaataa atatttccat ttaaatgtca amaaaaaaaa    811
ah                                                                  813
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<210> 294
<211> 778
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..576

<221> sig_peptide
<222> 154..360
<223> Von Heijne matrix
score 4.80000019073486
seq MMVLSLGIILASA/SF

<221> polyA_signal
<222> 737..742

<221> polyA_site
<222> 763..775

<400> 294
agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga 60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag 120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc 174
Met Thr Ser Gln Pro Val Pro
-65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
-60 -55 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
-45 -40 -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
-30 -25 -20 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
-10 -5 1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
5 10 15
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg 462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
20 25 30
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct 510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
35 40 45 50
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa 558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
55 60 65
tct tgt tct cct gtc ggg targataaca ggggttgctt rattttagat 606
Ser Cys Ser Pro Val Gly
70
caatttctta tcagactcaa ataaacattt cttttgaaaa tcatcttatt cttcacatta 666
tcatcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaaatc 726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaah cc 778

<210> 295
<211> 1060
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..897

<221> sig_peptide
<222> 154..360
<223> Von Heijne matrix
score 4.80000019073486
seq MMVLSLGIILASA/SF

<221> polyA_signal
<222> 1017..1022

<221> polyA_site
<222> 1044..1054

<400> 295
agtaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga 60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag 120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc 174
Met Thr Ser Gln Pro Val Pro
-65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
-60 -55 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
-45 -40 -35
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt 318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
-30 -25 -20 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
-10 -5 1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
5 10 15
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc 462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
20 25 30
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt 510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val
35 40 45 50
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg 558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu
55 60 65
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg 606
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu
70 75 80
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat 654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His
85 90 95
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct 702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala
100 105 110
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa 750
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa
115 120 125 130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc 798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
135 140 145
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm 846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly
150 155 160
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act 894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
165 170 175
tct taagaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata 947
Ser
tggaaaagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agcttttaaa 1007
gtaatgaaca ttaaaaaaaa ccattatttc actgtcaaaa aaaaaaamcc nkt 1060

<210> 296
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..292

<221> sig_peptide
<222> 146..253
<223> Von Heijne matrix
score 5.5
seq FTSMCILFHCLLS/FQ

<221> polyA_signal
<222> 395..400

<221> polyA_site
<222> 433..444

<400> 296
aacttgggac aagaratcaa actttaaaga tggtctaaag cccctcttaa aggtctgact 60
gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120
ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg 172
Met Gln Val Pro His Leu Arg Val Trp
-35 -30
aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca 220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
-25 -20 -15
agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa 268
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
-10 -5 1 5
aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt 322
Lys Lys Arg Lys Leu Xaa Leu Phe
10
tattgttgtt ttgctttttc tgccttcaaa ctactcccac aggccaaata tavctggctg 382
cttctttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa 442
aa 444

<210> 297
<211> 754
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 126..383

<221> sig_peptide
<222> 126..167
<223> Von Heijne matrix
score 7.5
seq VALNLILVPCCAA/WC

<221> polyA_signal
<222> 726..731

<221> polyA_site
<222> 743..754

<400> 297
aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaacttct 60
gctcgtttac actgcacatt gaatacaggt aactaattgg wwggagaggg gaggtcactc 120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg 170
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
-10 -5 1
tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct 218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
5 10 15
gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt 266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
20 25 30
tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga 314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
35 40 45
ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag 362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu
50 55 60 65
gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar 413
Gly His Arg Ile Cys Asp Leu
70
aaaccacagt cttcccagca attattacaa ttcttgaatt ccttggggat tttttactgc 473
ccttttcaaag cacttaaktg tkrratctaa cgtkttccag tgtctgtctg aggtgactta 533
aaaaatcaga acaaaacttc tattatccag agtcatggga gagtacaccc tttccaggaa 593
taatgttttg ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtatttaaaa 653
aaaagaaact tttctgaatg cctacctggc ggtgtatacc aggcagtgtg ccagtttaaa 713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaaa a 754

<210> 298
<211> 629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..497

<221> sig_peptide
<222> 66..239
<223> Von Heijne matrix
score 5.40000009536743
seq QLLDSVLWLGALG/LT

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 618..629

<400> 298
aactcccaga atgctgacca aagtgggagg agcactaggt cttcccgtca cctccacctc 60
tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg 110
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
-55 -50 -45
atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt 158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
-40 -35 -30
cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc 206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu

```
        -25                 -20                 -15
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca      254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
    -10                 -5                  1                   5
gtc ttt tcc acc act ggc cca gcc ctg ctg ctt ctg gtc agc ttc      302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe
                10                  15                  20
ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc      350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser
            25                  30                  35
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg      398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu
        40                  45                  50
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac      446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn
    55                  60                  65
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc      494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg
70                  75                  80                  85
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct           547
Ser
ccatccttgg gcctgakanc ccctccccac aactcagtgt ccttcaaata tacaatgacc    607
acccttcttc aaaaaaaaaa aa                                            629
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<210> 299
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..411

<221> sig_peptide
<222> 49..96
<223> Von Heijne matrix
score 10.1000003814697
seq LVLTLCTLPLAVA/SA

<221> polyA_signal
<222> 732..737

<221> polyA_site
<222> 750..763

<400> 299

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aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                                                    Met Glu Arg
                                                        -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
            -10                 -5                  1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
    5                   10                  15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20                  25                  30                  35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro
```

```
                40                  45                  50
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg      297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro
            55                  60                  65
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc      345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly
        70                  75                  80
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg      393
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
    85                  90                  95
ggc gag cat ccs rva btg tgaatkkkga ctttttctc ckccatttga             441
Gly Glu His Pro Xaa Xaa
100                 105
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcactgaatt tacaaaraca    501
gcaggaacrs ackggtgggg atgggcagct gttcrargcr atgggtkatc tgcccttcct    561
ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaatcgat    621
acagtgtatg acaatgtcat atagtataac acaacataat gaatataacg tgtatattgc    681
aacttaatat aatacgatgt aatataatgc tacataatac aacataatat aataaaatag    741
aatgcaacac aaaaaaaaaa aacc                                           765
```

<210> 300
<211> 623
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..534

<221> sig_peptide
<222> 49..96
<223> Von Heijne matrix
score 10.1000003814697
seq LVLTLCTLPLAVA/SA

<221> polyA_signal
<222> 593..598

<221> polyA_site
<222> 612..623

<400> 300

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aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                                                    Met Glu Arg
                                                        -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
            -10                 -5                  1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
    5                   10                  15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20                  25                  30                  35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
                40                  45                  50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
            55                  60                  65
```

```
atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
        70                  75                  80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
    85                  90                  95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100                 105                 110                 115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
                120                 125                 130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga          534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
            135                 140                 145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa    594
taaactctca tgcccccaaa aaaaaaaaa                                     623
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<210> 301
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 86..415

<221> sig_peptide
<222> 86..145
<223> Von Heijne matrix
score 9.80000019073486
seq FTIGLTLLLGXQA/MP

<221> polyA_signal
<222> 540..545

<221> polyA_site
<222> 560..571

<400> 301

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aaaaactcac ccagtgagtg tgagcattta agaagcatcc tctgccaaga ccaaaaggaa     60
agaagaaaaa bggccaaaag ccaaa atg ara ctg atg gta ctt gtt ttc acc      112
                          Met Xaa Leu Met Val Leu Val Phe Thr
                          -20                 -15
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc      160
Ile Gly Leu Thr Leu Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg
    -10                 -5                  1                   5
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt      208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu
                10                  15                  20
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat      256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp
            25                  30                  35
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc      304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe
        40                  45                  50
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat      352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp
    55                  60                  65
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct      400
```

```
Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser
70                  75                  80                  85
ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt      455
Gly Glu His His Ser
                90
tctagtttct atatagtgca atagagcata gattctataa attcttactt gtctaagaaa    515
gtaaatctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa       571


<210> 302
<211> 612
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..268

<221> sig_peptide
<222> 56..100
<223> Von Heijne matrix
      score 4.59999990463257
      seq LLTHNLLSSHVRG/VG

<221> polyA_signal
<222> 584..589

<221> polyA_site
<222> 601..612

<400> 302
ctaatcgaaa agggggattt tccggttccg gcctggcgag agtttgtgcg gcgac atg      58
                                                           Met
                                                           -15
aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg      106
Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
                -10                 -5                  1
tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc      154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
        5                   10                  15
cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg      202
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
    20                  25                  30
gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag      250
Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
35                  40                  45                  50
gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct             298
Val Pro Arg Arg Ala Gly
                55
gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccc tgcagtgccc    358
ggaatctgga cgtatgttcc ccatcagccg cgggatcccc aacatgctgc tgagtgaaga    418
ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg    478
ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac    538
accaaacaca gtgtttttga gctcggtatt atatattttt ttctcattaa aggtttaaaa    598
ccaaaaaaaa aaaa                                                     612


<210> 303
<211> 539
<212> DNA
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<213> Homo sapiens

<220>
<221> CDS
<222> 32..328

<221> sig_peptide
<222> 32..103
<223> Von Heijne matrix
score 4.59999990463257
seq FFIFCSLNTLLLG/GV

<221> polyA_signal
<222> 508..513

<221> polyA_site
<222> 528..539

<400> 303
aacaactatc ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga 52
Met Lys Ser Ala Lys Leu Gly
-20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg 100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
-15 -10 -5
ggt ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat 148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
1 5 10 15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt 196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
20 25 30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc 244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
35 40 45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt 292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg
50 55 60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg 338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg
65 70 75
tgaactcatg aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcaractg 398
atttwgaaat ctttgttwta tttccmymak ggcgwktaag cttccatatg tttgctattt 458
tcctgaccct agttttgtct ttcctggaaa ttaactgtat gakcattasa atgaaagagt 518
ctttctgtca aaaaaaaaaa a 539

<210> 304
<211> 964
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..527

<221> sig_peptide
<222> 21..95
<223> Von Heijne matrix
score 8.5
seq LKVLLLPLAPAAA/QD

<221> polyA_signal
<222> 921..926

<221> polyA_site
<222> 953..963

<400> 304
agggcggatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca 53
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
-25 -20 -15
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat 101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
-10 -5 1
tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac 149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr
5 10 15
caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc 197
Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr
20 25 30
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag 245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln
35 40 45 50
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc 293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys
55 60 65
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act 341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr
70 75 80
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt 389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys
85 90 95
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa 437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu
100 105 110
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc 485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr
115 120 125 130
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc 527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala
135 140
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgtccc tgggaggcca 587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca 647
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagaggaac aggaagagga 707
gggaaagcag gaagaaggac aggggactaa ggagggacgg gaggctgtgt ctcagctgca 767
gacagactca gagcccaagt ttcactctga atctctatct tctaaccctt cctcttttgc 827
tccccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat 887
tcgatcagcc caggaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag 947
aaaccaaaaa aaaaaak 964

<210> 305
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..647

<221> sig_peptide
<222> 147..374

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<223> Von Heijne matrix
      score 3.5
      seq LASASELPLGSRP/AP

<221> polyA_site
<222> 668..681

<400> 305
aacttcctgt gagcccggcg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg     60
acgacttctc ctrgrarmcc ccgactgagg cggagacgaa ggtgctgcag gcgcgacggg    120
agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac     173
                             Met Gly Asp Tyr Leu Leu Arg Gly Tyr
                                 -75                 -70
cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa      221
Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln
        -65                 -60                 -55
gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca      269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser
    -50                 -45                 -40
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc      317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser
-35                 -30                 -25                 -20
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc      365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly
                -15                 -10                 -5
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag      413
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu
            1                   5                   10
gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct      461
Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala
    15                  20                  25
gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg      509
Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu
30                  35                  40                  45
caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg      557
Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa
                50                  55                  60
gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg      605
Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg
            65                  70                  75
ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc              647
Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro
        80                  85                  90
tgagaaaaac ctctagaaaa acaaaaaaaa aaaaccc                             684



<210> 306
<211> 693
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 262..471

<221> sig_peptide
<222> 262..306
<223> Von Heijne matrix
      score 3.5
      seq LCFLLPHHRLQEA/RQ
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<221> polyA_signal
<222> 663..668

<221> polyA_site
<222> 682..693

<400> 306
atttcgcggc gctcgcbgma cyhsgwtgtt cagcaccttc ggtccggttg aggttgtcaa 60
gtcggmccaa acaggttgtt tctctgcagt ttccaacatg gcagggmsgt ttaatagaca 120
tggataagaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggta 180
aacacaaacg aaagaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat 240
cagtgacgtc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat 291
Met Ile Leu Cys Phe Leu Leu Pro His His
-15 -10
cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg 339
Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg
-5 1 5 10
gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa 387
Glu Lys Leu Arg Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys
15 20 25
raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga 435
Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly
30 35 40
gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg 481
Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp
45 50 55
ctgacccttt tgatttccaa vctcascgtt ttggtgtaag gcggccaaar aaggatgcgg 541
ascccagcac tgtgaagcct acaaaaacat tgatgcgctg gcttggggat ttgaatttga 601
acatctttca cactaagttc agactcatga aaccaatctt cagatgctct gtaaaccaca 661
taataaagag tttggaaatt aaaaaaaaar aa 693

<210> 307
<211> 1656
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..1216

<221> sig_peptide
<222> 74..172
<223> Von Heijne matrix
score 5.80000019073486
seq XLCLGMALCPRQA/TR

<221> polyA_signal
<222> 1627..1632

<221> polyA_site
<222> 1640..1652

<400> 307
atctcttggc gtctcaacgt tcggatcagc agctttttc cattctctct ctccacttct 60
tcagtgagca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag 109
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln
-30 -25
aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg 157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu
-20 -15 -10

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tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc      205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe
-5                  1               5                  10
acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt      253
Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg
            15                  20                  25
ttc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga      301
Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly
        30                  35                  40
act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc      349
Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly
    45                  50                  55
ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag      397
Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys
60                  65                  70                  75
ggt gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca      445
Gly Glu Thr Met Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro
                80                  85                  90
aat att gtt tgt agc aaa rat tac ttt gtc aca gca aac tcc aac cta      493
Asn Ile Val Cys Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu
            95                  100                 105
gtg att atc aca gca ggt gca cgc caa raa aag gga gaa acg cgc ctt      541
Val Ile Ile Thr Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu
        110                 115                 120
aat tta stc cag cga aat gtg gcc atc ttc aag tta atg att tcc agt      589
Asn Leu Xaa Gln Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser
    125                 130                 135
att gtc cag tac agc ccc cac tgc aaa ctg att att gtt tcc aat cca      637
Ile Val Gln Tyr Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro
140                 145                 150                 155
gtg gat atc tta act tat gta gct tgg aag ttg agt gca ttt ccc aaa      685
Val Asp Ile Leu Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys
                160                 165                 170
aac cgt att att gga agc ggc tgt aat ctg ata mhg gct cgt ttt cgt      733
Asn Arg Ile Ile Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg
            175                 180                 185
ttc ttg att gga caa aag ctt ggt atc cat tct gaa agc tgc cat gga      781
Phe Leu Ile Gly Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly
        190                 195                 200
tgg atc ctc gga gag cat gga gac tca agt gtt cct gtg tgg agt gga      829
Trp Ile Leu Gly Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly
    205                 210                 215
gtg aac ata gct ggt gtc cct ttg aag gat ctg aac tct gat ata gga      877
Val Asn Ile Ala Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly
220                 225                 230                 235
act gat aaa gat cct gag caa tgg aaa aat gtc cac aaa gaa gtg act      925
Thr Asp Lys Asp Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr
                240                 245                 250
gca act gcc tat gag att att aaa atg aaa ggt tat act tct tgg gcc      973
Ala Thr Ala Tyr Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala
            255                 260                 265
att ggc cta tct gtg gcc gat tta aca gaa agt att ttg aag aat ctt     1021
Ile Gly Leu Ser Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu
        270                 275                 280
agg aga ata cat cca gtt tcc acc ata act aag ggc ctc tat gga ata     1069
Arg Arg Ile His Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile
    285                 290                 295
rat gaa gaa gta ttc ctc agt att cct tgt atc ctg gga gag aac ggt     1117
Xaa Glu Glu Val Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly
300                 305                 310                 315
att acc aac ctt ata aag ata aag ctg acc cct gaa gaa gag gcc cat     1165
Ile Thr Asn Leu Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His
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                320                 325                 330
ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag    1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys
            335                 340                 345
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata         1266
Leu
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaag  1326
taggtagagt gattttccta tttatttagt cctccagctc ttttattgag catccacgtg  1386
ctggacgata cttatttaca attcckaagt atttttggta cctctgatgt agcagcactt  1446
gccatgttat atatatgtag ttgrmatttg gttcccaaaa agtaggatgt aggtatttat  1506
tgtgttctag aaattccgac tcttttcatt agatatatgc tatttctttc attcttgctg  1566
gtttatacct atgttcattt atatgctgta aaaaagtagt agcttcttct acaatgtaaa  1626
aataaatgta catacaaaaa aaaaaamcmc                                   1656


<210> 308
<211> 517
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..164

<221> sig_peptide
<222> 48..89
<223> Von Heijne matrix
      score 4
      seq YYMVCLFFRLIFS/EH

<221> polyA_signal
<222> 482..487

<221> polyA_site
<222> 505..517

<400> 308
aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac      56
                                                Met Tyr Tyr
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att     104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
    -10                 -5                  1               5
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca     152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
                10                  15                  20
aca tct gct ggc taaataaaga catgatcttc acctttggg attgttaatt          204
Thr Ser Ala Gly
            25
taaaatggtt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctggtg   264
atttatatgg ctcttcacaa ggtgttattt tggggtatca aggtatggat gcttaaatca   324
gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg   384
gtccttccac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct   444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg   504
aaaaaaaaaa aaa                                                      517


<210> 309
<211> 405
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 185..334

<221> sig_peptide
<222> 185..295
<223> Von Heijne matrix
score 5.90000009536743
seq LSYASSALSPCLT/AP

<221> polyA_signal
<222> 355..360

<221> polyA_site
<222> 392..405

<400> 309
atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccctc tcctgacctg 60
cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct 120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
-35 -30 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
-20 -15 -10
ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg 325
Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
-5 1 5 10
cct gac aac taaatatcct tatccaaatc aataaarwra raatcctccc 374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaa a 405

<210> 310
<211> 1087
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 195..347

<221> sig_peptide
<222> 195..272
<223> Von Heijne matrix
score 7.09999990463257
seq LASLQWSLTLAWC/GS

<221> polyA_signal
<222> 1037..1042

<221> polyA_site
<222> 1071..1082

<400> 310
aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt 60
acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg 120
gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgaccc agttgctggc 180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg 230